

One of skill in the art will appreciate that the order of the individual antigens within the fusion protein may be changed and that comparable activity would be expected provided each of the epitopes is still functionally available. In addition, truncated forms of the proteins containing active epitopes may be used in the construction of fusion proteins.

3

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Reed, Steven G.
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- (ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
- (iii) NUMBER OF SEQUENCES: 214
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SEED and BERRY LLP
 - (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: USA
 - (F) ZIP: 98104-7092
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 01-OCT-1997
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Maki, David J.
 - (B) REGISTRATION NUMBER: 31,392
 - (C) REFERENCE/DOCKET NUMBER: 210121.411C7
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGCACCG	GTAGTTTGAA	CCAAACGCAC	ATTGACGGG	CAAACGAACG	GAAGAACACA	60
ACCATGAAGA	TGGTGAAATC	GATCGGCGCA	GCTCTGACCG	CCGCGGCTGC	AATCGGCGCC	120
GCTCGGCGCG	GTGTGACTTC	GATCATGGCT	GGCGGCGCGG	TGGTATACCA	GATGCAGGCG	180
GTGGTCTTCG	GCGGCGCACT	GCGGTTGAGC	CCGGCATCCG	CCCGTGACGT	CCCGACCGCG	240
CCCCAGTTSA	CCAGCCTGCT	CACAGGCTC	CCCGATCCCA	ACGTGTCGTT	TGCGAACAAG	300
GKCAETCTGG	TGAGGCGCGG	CATCGGGGGC	ACCGAGGCGC	GCAICGCGGA	CCACAAGCTC	360
AAGAAGGCCG	CCGAGCAGCG	GGATCTGCGG	CTGTCTGTTA	GCTGAGCGAA	CATCCAGCGG	420
GCGGCGCGCG	GTTCGGGCAC	CGCGGACGTT	TGGTCTCGCG	GTCCGAAGCT	CTGCTCGCGG	480
GTCAGCCASA	ACCTCAGGTT	GCTGAATCAA	CGCGGCTGGA	TGCTGTACCG	CGCATCGGCG	540
ATGGAGTTGC	TGAGGCGCGC	AGGGNAACTG	ATTGGCGGGC	CGGNTTCAGC	CGGCTGTTCA	600
GCTACGCGCG	CGGCTGCTG	ACGGGTCCAT	GTCGAACACT	CGGCGTGTGA	GCACGGTGGG	660
GTNTGCGCAG	GGGCGCAGCG	ACGCGCGCGT	GCAAGCGGTC	CTCGAGATAG	GTGGTGNCTC	720
GNCACGAGCG	AMCAGCGCGG	NTTGGGCGGT	TCTCGTGTGT	GNATGA		766

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCATCACC	ATCACCATCA	CGATGAAGTC	ACGGTAGAGA	CGACCTCGGT	CTTCCGCGCA	60
GACTTCCTCA	CGGAGCTGGA	CGCTCCTCGG	CAAGCGGGTA	CGGAGAGCGC	GCTCTCCGGG	120
GTGGAAAGGCG	TCCCGCGCGG	CTCGGCGTTG	CTGGTAGTCA	AACGAGGCCC	CAACCGCGGG	180
TCCCGGTTCC	TACTCGACCA	AGCCATCAAG	TGGGCTGGTC	GGCATCCCGA	CAGCGACATA	240
TTCCTCGAGC	ACGTGACCGT	GAGCCGTCCG	CATGCTGAAT	TCCGGTTGGA	AAACAACGAA	300
TTCAATGTGC	TGATGTGCG	GATGTCAAC	GGCACTACG	TCAACGCGGA	GCGGTTGGAT	360
TGGGCGGTGC	TGGGGAACCG	CGACGAGGTC	CAGATCGGCA	AGCTCCGGTT	GCTGTTCTTG	420
ACCGGACCCA	AGCAAGGCGA	GGATGACGGG	AGTACGCGGG	GCCCGTGAGC	GCACCGGATA	480
GCCCGCGGCT	GGCGGGGATG	TGATCAGCGG	CGGTCTCGCG	ACCTGCTACG	ACCGGATTTT	540
CCCTGATGTC	CACCATCTCC	AAGATTGAT	TCTGGGAGG	CTTGAGGCTC	NGGCTGACCC	600
CCCCCGGGG	CTCATTCGCG	GGTTCGCGG	GTTTTCACCC	CATACCNACT	GCCNCGCGGN	660

TTGCNAATTC NTTCTTCTCT GGCNNAAAG GGACCTTTAN CTTGCCGCTN GARANGGTNA 720
 TCCNGGGCCC NTCTTNGAAN CCCCNTCCCC CT 752

(2) INFORMATION FOR SEQ ID NO:3:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 813 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCATC ACCATCACCA TCACACTTCT AACCGCCAG CGCGTCCGGG GCSTCGAGCA 60
 CCACGGGACA CCGGGCCCGA TCGATCTGGT AGCTTGAGTC TGCTCAGSCA TCTCTCTCAG 120
 CAGCGCGATG CCGTATGTTT GTCTCTGACT CAGATATCGC GGCATCCAA TCTCCCGCTT 180
 GCGGCGGGGG GTGCTGCAAA CTACTCCGGG AGGAATTTGG ACCTGCCCAT CAAGATCTTC 240
 ATGCTGGTCA CGGCTGTCTT TTTGCTCTGT TGTTCGGGTG TGGCCACGGC CGGCGCCAAAG 300
 ACCTACTGGG AGGAGTTGAA AGGACCCGAT ACCGGCCAGG CGTGGCAGAT TCAAATGTCC 360
 GACCGCGCTT ACAACATCAA CATCAGCTTG CCCGTTACT ACCCGACCA GAATGCGCTG 420
 GAAATTTACA TCGCCAGAC GCGGACAAAG TTCCTCAGCG CGGCCACATC GTCCACTCCA 480
 CGCGAAGGCC CCTACGAATT GATATCACC TCGGCTACAT ACCAGTCCGC GATACCGCCG 540
 CGTGGTACGC AGGCGGTGGT GCTCAGGCTC TACCACACCG CCGGCGGCAC GCACCCACG 600
 ACCAGTACA AGGCTTTGGA TTGGGACCAAG GCCTATCGCA AGCCAAATCAC CTATGACACG 660
 CTGTGGCAGG CTGACACCGA TCGGCTGCCA GTCTCTTCC CCATTCTTCC AAGGTGAAT 720
 GAGCAACGCA GACCGGGACA ACWGGTATCG ATAGCGGCN AATGCCGCTT TGGACCCNG 780
 TGAATTTATC ACAACTTCCG AGTCACNAA NNA 813

(2) INFORMATION FOR SEQ ID NO:4:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAC ACGGCCGCT CCGATAACTT CCAGCTGTCC CAGGCTGGGC AAGGATTCGC 60

CATTCCGATC	GGGCAGGCGA	TGGCGATCUC	GGGCCAGATC	CGATCGGGTG	GGGGGTCACC	120
CACCGTTCAT	ATCGGGCCCTA	CGGCGTTCCT	CGGCTTGGGT	GTTGTCGACA	ACAACGGCAA	180
CGGCGACGSA	GTCCAACGCG	TGGTCGGGAG	CGCTCGGGCG	GCAAGTCTCG	GCATCTCCAC	240
CGGCGAGCTG	ATCACCAGCG	TGSACGGGCG	TCCGATCAAC	TGSGCCACCG	CGATGGCGGA	300
CGGCGTTAAC	GGGCATCATC	CGGCTGACCT	CATCTGGGTG	AACTGSCAAA	CCAAGTCGGG	360
CGGCACGCTT	ACAGGGAACG	TGACATTGGC	CGAGGGACCC	CGGGCTTCTT	TTCTCTGCGG	420
ATACCACCCG	CGGCGGGGCG	AATGGGA				447

(2) INFORMATION FOR SEQ ID NO:5:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 604 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCCACTGC	GGTCGGCGAG	TATGTCGCCC	AGCAAATGTC	TGGCAGCCGC	CCAACGGAT	60
CCGCTGATCC	GACGTGCGAG	GTTGTCGAAC	CCGCTGCCCC	GGAAGTATCG	GTCCATGCCT	120
AGCCCGGCGA	CGGCGAGCGC	CGCAATGGCG	CGAGTGAGGA	GGCGGGCAAT	TTGGCGGGGC	180
CGGCGAGCGG	AGAGCGCGCG	AATGGCGCGA	GTCAGGAGGT	GGCAAGTCAT	GGCCAGNGTC	240
ATCCAATCAA	CCTGATTCG	GNCTGNGGCG	GCATTTGACA	ATCGAGGTAG	TGAGCGGAAA	300
TGAATGATCG	AAACCGGGNG	GNGACGTCGG	NTCTTCTGGT	GGTGNTAGGT	GNCTGNTCTGG	360
NGTNGNGGNT	ATCAGGATGT	TCTTCGNCGA	AAGCTGATCG	CGAGGAACAG	GGTGTNCCCG	420
NNANNCCNAN	GGGTCNAN	CCNNNNNTCC	TGNCNANAT	CANANAGNCG	NTTGATNGCA	480
NAAAAGGGTG	GANCAGNNNN	AANTNGNGGN	CCNAANAANC	NNNANNGNNG	NNAGNTNGNT	540
NNNTNTTNNC	ANNNNNNNTG	NNGNNGNNGN	NNNCAAMCNC	NTNNGNGMAA	NNGGNTTNTT	600
NAAT						604

(2) INFORMATION FOR SEQ ID NO:6:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 633 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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TTGCAGCTCG AACACCTCA CTAAAGGGA CAAAGCTNG AGCTCCACCG CGGTGGGCGC 60
CGCTCTAGAA CTAGTGNATH YYYCKGGGTG CAGGAATYCG GYACGAGCAT TAGGACAGTC 120
TAACGGTCTCT GTTACGGTGA TCGAATGACC GACGACATCC TCGTGATCGA CACCGACGAA 180
CGGGTGCAGAA CCTCACCCT CAACCGGCTG CAGTCCCGYA ACGCGCTCTC GGCGGCGGTA 240
CGGGATCGST TTTTCGGGY GTTGGYCGAC GCGGAGGYCG ACGACGACAT CGACGTCTCT 300
ATCCTCAGCG GYCCCGATCC GGTGTTCTGC GCGGACTGG ACCTCAAGGT AGCTGGCCGG 360
GCAGACCGCG CTGCGGACA TCTCAGCGCG GTGGGCGGCG ATGACCAAGC CGGTGATCGG 420
CGCGATCAAC GCGCGCGCG TCACCGCGCG GCTCGAAGTG GCGCTGTACT GCGACATCTT 480
GATGGCTTCC GAGCAGCGCG GTTCCGCGA CACCGACGCG CGGTGCGCG TCGTGGCCAC 540
CTGGGGAGTC AGTGTGTCT TCGCGCAAAA GGTGGGATC GGNCTGGGCG GGTGATGAG 600
CCTGACCGGC GACTACCTGT CCGTGACCGA CGC 633

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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CGACGACGAC GCGCGCGGAG AGCGGGCGCG AACCGCGATC GACGCGGCGC TGCCAGAGT 60
CGGCACCAAC CAGGAGGAG TCGAATCATG AAATTGTCA ACCATATTGA GCGGCTCGCG 120
CGCGCGCGAG CGCGCGGCG GGTGCGCGAG GTCTATGCG AGCGCGGCG CGAGTTGCG 180
CGGTGCGCG AGCGGCTCG CATGCTGTCC CGGAGGAG GACTGCTCAC CGCGGCTGG 240
GGGACGTTCC GCGAGACACT GCTGCTGCG CAGGTGCGCG GTGGCGGCA GAGAGCGGTC 300
GCGCGCGCG TCGCGGCG CCGTGGCTGC CCTGCTGCG TCGAGGACA CACGACATG 360
CTGTACCGCG CAGGCGAAG CGACACGCG GCGCGATCT TCGCGGCG AGCAGCTGCC 420
GCGGCTGACC CGAACCGCG GTATGTGCG TGGCGGCGAG GAACCGGAG ACCCGCGGGA 480
CGGCGGCGAC CGTTGCGCG GATGTGCG GCGAATACC TGGGCGGCG GGTGCAATTC 540
CAGTTCATCG CAGGCTGCT CCTGCTGCT CTGAGGAAA CTTGCTGCG GCGCGGCGCG 600
CGCGCGCAAC AGCTCATGCG CGCGCGCGGT GAGTGTGT TCGCGCGCAA GTGCGCGCG 660
GAGCATCGCG CGCGCGGCT CACCGCGCG CTGAGCGCG GAGGCTGCG CGACGATCTG 720

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GCATGGGCAA	CACCGTCGGA	GCCCATAGCA	ACCGCCTTCG	CCGCCCTCAG	CCACCACTTG	780
GACACCGGCG	CSCACCTGCC	GCCACCGACT	CGTCAGGTGG	TCAGGCGGGT	CGTGGGCTGG	840
TGGACGGGCG	AGCCAATGCC	GATGAGCAGT	CGCTGGACGA	ACGAGCAGAC	CCCCGAGCTG	900
CCCGCCGACC	TGCACGCGCC	CACCCGTCTT	GCCTTGCTGA	CCGGCCTGGC	CCCGATTCAG	960
GTGACCGAGC	ACGACGTCGC	CGCGGCCCGA	TCCCTGCTCG	ACACCGATGC	GGCGCTGGTT	1020
GGCGCCCTGG	CCTGGGCGGC	CTTCACCGCC	GCGCGGCGCA	TGGGCACCTG	GATCGGCGCC	1080
GCCGCGGAGG	GCCAGGTGTC	GCGGCAAAAC	CGACTGGGT	GATGTTCGCG	GCCCTGTGGG	1140
TAGGCTGTCA	TCCCTGGCCC	GAGGATCTTC	GCGGCGGCGA	ACGGAGGTGG	CGACACAGGT	1200
GGAAGCTGGG	CCCACTGGCT	TGCGCGCCAA	CCCGCTCGTG	GCGTTTCGGT	TGGCGGCACT	1260
GGCGATTCAG	GTGCGGCGCG	GCCCTTGGCC	GAAGTCCAG	CTCAACGTGC	CGTCACCGAA	1320
GGACCGGAGC	GTCACCGGGG	GTCACTCTGC	GCGCCCAAGG	AA		1362

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1458 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGAGGACCC	CGATATGGCG	GCCACCGTAG	CGAAGCCGCT	CGCCGAGCGA	CTCGGCGCGG	60
GTATCGCTCC	CGTTGAGGAC	ATTCAGGACT	GCGTGGAGGC	CCGGCTGGGG	GAAGCCGGTC	120
TGGATGAGCT	GGCCCGTGT	TACATCATCT	ACCGGCGAGC	GCGCGCCGAG	CTGGCGACGG	180
CTAAGGCTTT	GCTCGGCTG	CGGACCGAGT	TAAAGCTGAG	CTTGGCGGCT	GTGACCGTAC	240
TGGCGGAGCG	CTATCTGCTG	CACSACGAGC	AGGCGCGGCG	GCGCGAGTGG	ACCGCGGAGC	300
TGATGGACCG	ATCGGCGCGC	TGTGTGCGCG	CGGCGGAGGA	CCAGTATGAG	CCGGGCTCGT	360
CGAGGCGGTG	GGCGGAGCGG	TTCGCGACGC	TATTACGCAA	CCTGGAATTC	CTGCGGAATT	420
CGCCACGCTT	GATGAAGCTT	GGCACCGACC	TGGGACTGCT	CGCGGCTGCT	TTTGTCTCTG	480
CGATTCAGGA	TTCGCTGCAA	TGGATCTTTC	CGAGCTGGGG	ACAGGCGGCG	GAGCTGCAGC	540
GCGCTGGAGG	CGGACCGGGA	TATGCGTTCA	GCCACCTGGG	ACCGCGCGGG	GATCGGGTGG	600
CCTCCACGGG	CGGACCGGCT	AGCGGACCGG	TGTGCTTTCT	ACGGCTGTAT	GACAGTGGCG	660
CGGCTGTGGT	CTCCATGGGG	GCTGCGCGGC	GTGGCGGCTG	TATGGCTGTG	CTTGAATGCT	720
CGACCGCGGA	TATCTGTGAT	TTCGTCACCG	CGAGGCGGGA	ATCGCGCGGC	GAGCTCCGCG	780

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ATFTCAACCT ATCGGTTGGT GTGACCGACG CGTTCTCTGG GGCCTTCGAA CGCAACGSGC      840
TACACCGGCT GGTCAATCGG CGAACCGGCA AGATCGTGGG GCGGATGCCC GCGGCGGAGC      900
TGTTCGACGC CATCTGCAAA GCCCGGCAAG CGGCTGGCGA TCCCGGGCTG GTGTTTCTCG      960
ACACGATCAA TAGGGCAAC CCGGTGCCCG GGAGAGGCCC CATCGAGGCG ACCAACCCTT     1020
GCGGGGAGGT CCCACTGCTG CTTACGAGT CATGYAATCT CGGCTCGATC AACCTCGCCC     1080
GGATGCTGSC CGACGGTGGC GTGGACTGGG ACCGGCTCGA GGAGGTGCCC GGTGTGGCGG     1140
TCCGGTTCTT TGATGACGTC ATCGATGTCA GCGGCTACCC CTTCCTCGAA CTGGGTGAGG     1200
CGGCCCCGCG CACCCGCAAG ATCGGGCTGG GATCATGGG TTTGGCGGAA CTGCTTGGCG     1260
CACTGGGTAT TCCGTAGGAC AGTGAAGAAG CGGTGCGGTT AGCCACCGGG CTCATGCGTC     1320
GCATACAGCA GCGGGCGCAC ACCGCATGCG GGAGGCTGGC CGAAGAGCGG GCGGCATTCC     1380
CGGCGTTTAC CGATAGCCGG TTCGCGCGGT CGGCGCCGAG GCGCAACGCA CAGGTCACTT     1440
CGGTGCTCC GACGGGCA

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1458

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 862 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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ACGGTGTAAAT CGTGTGGAT CTGGAACCGC GTGGCCCGCT ACCTACCGAG ATCTACTGGC      60
GGGCGAGGGG GGTGGCCCTG GGCATCGCGG TCGTCGTAGT CCGGATCGCG GTGGGCATCG     120
TCATCGCCCTT CTTGACAGAC AGCGCCGGTG CCAGAACCGGT CAGGSCCGAC AAGCCGGGCTT     180
CGCCCCAGAG CCATCCGGGG TCGCCGBCAC CCCAAGCACC CCAGCCGGCC GGGCAAAACG     240
AAGGTAAAGC CGCCCGGGCC CGGCGCGAGG GCGAARACCC CGAGACACCC ACGCCACCG     300
CGCGGGTGCA GCGGCGGCGG GTGCTCAAGG AAGGGGACGA TTGCCCCGAT TCGACGCTGG     360
CCGTCAAAGG TTTGACCAAC GCGCGCGAGT ACTACGTGGG CGACCGGCGG AAGTTCAACCA     420
TGGTGGTAC CAACATCGGC CTGGTGTCTT GTAAACGCGA CTTTGGGCCC GCGGTGTGG     480
CGGCTTACGT TTTACTGCTG GACAACAAGC GGTGTGTGTC CAACCTGGAC TGGCGGCCCT     540
CGAATGAGAC GCTGGTCAAG ACCTTTTCCC CCGGTGAGCA GGTAAAGACC GCGGTGACCT     600
GGACCGGGAT GGGATCGGGG CCGCGCTGCC CATTGCCGCG GCGGCGGATC GGGCGGSCA     660
CCTACAAATCT CGTGGTACAA CTGGGCATC TCGGCTCGCT GCGGCTTCCG TTCACTCTGA     720

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ATCAGCCGCC GGGGGCGGCC GGGCCGGTAC CCGCTCCGGC TCCAGCGCAG GCGGCTCCGC      780
CGGAGTCTTC CGGCGAAGGC GGATAATTAT TGAATCGCTA TGGTCGATTG CCGCAGCTGT      840
GACAACCCCT CGCCTCGTGC CG                                     862

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(2) INFORMATION FOR SEQ ID NO:10:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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TTGATCAGCA CCGGCAAGGC CTCACATGCC TCCCTGGGTG TGCAGGTGAC CAATGACAAA      60
GACACCCCGG GCGGCAAGAT C CTCGAAGTA GTGGCCGGTG GTGCTGCGGC GAACCTCGA      120
GTGCGGAAGG GCGTGGTTGT CACCAAGSTC GAGGACCGGC CGATCAACAG CCGCGACGCG      180
TTGGTTGCCG CGTSGCGGTC CAAAGGCGCG GCGGCCACCG TGGCGCTAAC CTTTCAGGAT      240
CCTTCGGGCG GTACCCGCAC AGTGCAAGTC AGCCTCGGCA AGGCGGAGCA GTGATGAGG      300
TGCGCCGCGC GTGTTCAAAG CTCGGATATA CGGTGGCACC CATGGAACAG CGTGCAGACT      360
TGGTGGTTGG CCGGGCACTT GTCTCGTTCG TTGACGATCG CACGGCGCAC GCGGATGAAG      420
ACCACAGCGG GCGGCTTGTC ACCGAGCTGC TCACCGAGGC CGGCTTTGTT GTCCAGCGCG      480
TGCTGCGCGT GTGGGCGGAC GAGGTGAGAG TCGGAAATGC CCTGAACACA GCGGTGATCG      540
GCGGGGTGGA CTTGCTGGTG TCGGTGCGCG GGACCGGNGT GACGCTCGCC GATGTCACCC      600
CGGAAGCCAC CCGGACATT CT                                     622

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(2) INFORMATION FOR SEQ ID NO:11:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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GGCGCAGCGG TAGGCTGTT GAGCGCCGCG ACACTGGTGT TGACAGCATG CCGCGGTGGC      60
ACCAACAGCT CGTCGTCAGG CGCAGGCGGA ACCTGTGGGT CCGTGCACAG CCGCGGCAAG      120
AAGGAGCTCC ACTCCAGCGG CTCGACCGCA CAGGAAATG CCATGGAGCA GTTCGTCTAT      180

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GCCTACGTGC	GATCGTGC	GGCTACACG	TTGGACTACA	ACGCCAACGG	GTCCGGTGGC	240
GGGGTGACCC	AATTTCTCAA	CAACGAAACC	GATTTCCGCC	GCTCGGATGT	CCCCTTGAAT	300
CCCTCGACCG	GTCAACCTGA	CGGCTCGGCG	GAGCGGTGCG	GTTCCTCCGG	ATGGGACCTG	360
CCGACGGTGT	TGCGCCCGAT	CGCGATCACC	TACATATCA	AGGGGCTGAG	CACGCTGAAT	420
CTTGACGGAC	CCACTACCGC	CAAGATTTTC	AACGGCACCA	TCACCGTGTG	GAATGATCCA	480
CAGATOCAG	CCCTCAACTC	CGGCACCGAC	CTGCCGCCAA	CAGCGATTAG	CGTTATCTTC	540
CGCAGCGACA	AGTCCGGTAC	GTGGGACAA	TTCCAGAAAT	ACCTCGACGG	TGTATCCGAC	600
GGGGCGTGGG	GCAAAGGCGC	CAGCGAAACG	TTCAGCGGGG	GCTCGGGCT	CGGCGCCGCG	660
GGGAACAACG	GAACGTGGC	CCTACTGCAG	ACGACCGACG	GGTCCATCAG	CTACAACGAG	720
TGGTCGTTTG	CGGTGGGTAA	GCASTTGAAC	ATGGGCCAGA	TCATCAGTTC	GGCGGGTCCG	780
GATCCASTGG	CGATCACCAC	CGASTCGGTC	GGTAAGACAA	TCCCGGGGGC	CAAGATCATG	840
GGACAAGGCA	ACGACCTGGT	ATGAGACAG	TGCTCGTTCT	ACAGACCCAC	CCAGCCTGGC	900
TCTTACCCGA	TGCTGCTGGC	GACCTATGAG	ATGCTCTGCT	CGAAATACCC	GGATGCGAGC	960
ACGGGTACTG	CGGTAGGGC	GTTTATGCAA	GCGGCGATTG	GTCCAGGCCA	AGAAAGGCTG	1020
GACCAATACG	GCTCCATTCC	GTTGCCCAAA	TCGTTCCAGG	CARAATTGGC	GGCCCGGGTG	1080
AATGCTATTT	CTTGACCTAG	TGAGGGGAAT	TGACCGGTGA	CGGATGCCCT	TCCGCAAGTA	1140
GGCTCGCAAT	TGCGCCGTA	TCAGCTATTG	CGGCTGCTGG	GCCGAGGCGG	GATGGGCGAG	1200

(2) INFORMATION FOR SEQ ID NO:12:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1155 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAAGCAGCT	GCAGGTCTTG	CTGTTGACG	AACTGGGCAT	GCCGAGGAC	AAAGCACCA	60
AGACCGGCTA	CACCAAGGAT	GCCGACGCG	TGCACTCGTT	GTTCCACAG	ACCGGGCATC	120
CGTTTCTGCA	ACATCTGCTC	GCCACCGCG	ACCTACCGG	GCTCAAGGTC	ACCGTGACG	180
GGTTGCTCCA	AGCGGTGGCC	GCCGACGGC	GCAATCACAC	CACGTTCAAC	CAGACGATCG	240
CCCGGACCGG	CGGCTCTCC	TGACCGAAC	CCAACTGCA	GAACATCCCG	ATCCGACCGG	300
ACCGGGGCGG	GCGGATCCGG	GACGCTTGG	TGCTCGGGGA	CGGTTACGCG	GAGTTGATGA	360
CGGCGACTA	CAGCCAGATC	GAGATGCGGA	TCATGGGGCA	CCTGTCGGGG	GACGAGGGCC	420

TCATCGAGGC	GTTCAACACC	GGGAGGACC	TGTATTCGTT	CCTCGCGTCC	CGGCTGTTCC	420
GTGTGCCCAT	CGACGAGGTC	ACCGGCGAGT	TCCGGCGCCG	GCTCAGGCG	ATGTCTTACG	540
GGTCTGTTTA	CGGGTTGAGC	GCTACGGCC	TGTCCGAGCA	GTTGAAAATC	TCCACCGAGG	600
AAGCCAACGA	GCACATGGAC	GCGTATTTCC	CCCGATTCCG	CGGGGTGCC	GACTACCTGC	660
GCGCCGTAGT	CGAGCGGGCC	CGCAAGGACC	GCTACACCTC	GACGGTGGC	GCCCGTCGCC	720
GCTACCTGCG	CGAGCTGGAC	AGCAGCAACC	GTCAAGTCCG	GGAGGCGGCC	GAGCGGCGCG	780
CGCTGAACGC	GCCGATCCAG	GCCAGCGCGG	CCGACATCAT	CAAGGTGGCC	ATGATCCAGG	840
TCGACAAGGC	GCTCAACGAG	GCACAGCTGG	CGTCGGCAT	GCTGCTGCG	GTCACCGACG	900
AGCTGCTGTT	CGAAATCCCC	CCCGGTGAAC	GCGAGCGGGT	CGAGGCCCTG	GTGCGCGACA	960
AGATGGGCGG	CGCTTACCGG	CTCGACGTCC	CGGTGGAGGT	GTGGGTGGGC	TACGGCGGCA	1020
GCTGGGAGGC	GGCGGCGCAC	TGAGTCCCGA	GCTGCGATCT	GGGCGGGGAA	TTCGGCGATT	1080
TTTCCGCCCT	GATTCACGC	TGGCGCGAAT	CGGACCGAG	TTTGTCCAGC	GTGTACCGGT	1140
CGAGTAGCCT	CGTCA					1155

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGCGGTC	TGGTCTTTGA	ACGGTTTTAC	CGTCCGCAAT	CGGCAGGGCC	CTTGCCGGGT	60
TGGGGCCTCG	GCTTGGCGAT	GCTCAACAG	GTCGTCTCA	ACCACGGCGG	ATTGCTGGGC	120
ATCGAAGACA	CGACCCAGG	CGGCCAGGCC	CCTGGAACGT	CGATTTACGT	GCTGCTCCCC	180
GGCGGTCGGA	TGCCGATTCC	GCAGCTTCCC	GGTGGGACGG	CTGGCGCTCG	GAGCAAGGAC	240
ATCGAGAACT	CTGGGGTTC	GGCGAACGTT	ATCTCACTGG	AATCTCAGTC	CACGCGCGCA	300
ACCTAGTTGT	GCAGTTACTG	TTGAAAGCCA	CACCATGCC	AGTCCACGCA	TGGCCAASTT	360
GGCCCGAGTA	GTGGGCGTAG	TACAGGAAGA	GCAACCTAGC	GACATGACCA	ATCACCCAGC	420
GTATTGCCCC	CCGCCGAGC	AGCCGGAAC	CCGAGTTAT	GCTCAGGGGC	AGCAGCAAC	480
GTCAGGCCAG	CAGTTGCACT	GGCGTTACCC	ACGCTCCCGG	CCCCCGCAGC	CAACCCAGTA	540
CGGTCAACCC	TACGAGCGGT	TGGGTGGTAC	CCGGCCGGGT	CTGATACCTG	GCGTGTATCC	600
GACCATGAGC	CCCCCTCCTG	GGATGCTTCG	CGACGCGCCT	CCTGCAGGCA	TGTTGGCCAT	660

CGGCGCGGTE	ACGATAGGCG	TGGTGTCCGC	GGGATCGGEC	GGCGCGGCGG	CATCCCTGGT	720
CGGGTTCAAC	CGGGCACCGG	CTGGGCCCAG	CGCGGGCCCA	GTGGCTGCCA	GGCGGCGCGG	780
AAGCATECCC	GCAGCAACA	TGCGCGCGGG	GTGGGTGGAA	CAGGTGGCGG	CCAAGGTGGT	840
GCCCASTGTC	GTGATGTTGG	AAACCGATCT	GGCGCGCGAG	TGGGAGGAGG	GCTCGGGCAT	900
CATTCTGTCT	GGCGAGGGGG	TGATTTTGAC	CAACAACGAC	GTGATCGCGG	CGCGCGGCCA	960
GGCTCCCTTG	GGCASTCGCG	CGCGCAAAAC	GACGGTAACC	TTCTCTGACG	GGCGGACCGC	1020
ACCGTTCAAG	GTGGTGGGGG	CTGACCCGAC	CAGTGATATC	GGCGTCGTCC	GTGTTGAGGG	1080
CGTCTCGGGG	CTCACCCCGA	TCTCCCTGGG	TTCTCTCTCG	GACCTGAGGG	TGGGTGAGCC	1140
GGTCTGCGCG	ATCGGGTCCG	CGCTCGGTTT	GGAGGGCACC	GTGACCACGG	GGATCCTCAG	1200
CGCTCTCAAC	CGTCCAGTGT	CGACGACCGG	CGAGGGCGGC	AACGAGAACA	CGTCTCTGGA	1260
CGCCATTGAG	ACCGACGCGG	CGATCAACCC	CGGTAACCTC	GGGGGCGCGC	TGGTGAACAT	1320
GAACGCTCAA	CTCGTCCGAG	TCAACTCGGC	CATTGCCACG	CTGGGGCGCG	ACTCAGCCGA	1380
TGCGCAGAGC	GGCTCGATCG	GTCTCGGTTT	TGCGATTCCA	GTGACCAGGG	CCAAGCGCAT	1440
CGCGGACGAG	TGATCAGCA	CGGGCAAGGC	GTGACATGCC	TCCCTGGGTG	TGGAGGTGAC	1500
CAATGACAAA	GACACCCCGG	GGCCCAAGAT	CGTCGAATTA	GTGGGCGGTG	GTGCTGCCGC	1560
GAACGCTGGA	GTGCCGAAGG	GCGTCGTTGT	CACCAAGGTC	GACGACCGCC	CGATCAACAG	1620
CGCGGACGCG	TGGGTGCGCG	CGTSCGGTTC	CAAGGCGCGG	GGGGCGACCG	TGGCGCTAAC	1680
CTTTCAGGAT	CGCTCGGGCG	GTAGCCGAC	AGTGCAAGTC	ACCGTCGGCA	AGCGGAGCA	1740
GTGATGAAGG	TGCGCGCGCA	GTGTTCAAG	C			1771

(2) INFORMATION FOR SEQ ID NO:14:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCCACCCCG	GTGGCGGCGG	CTCTAGAACT	AGTGCAATCC	CGGGGCTGCA	GGAATTCGGC	60
ACGAGGATCC	GACGTGCGAG	GTGTGCGAAC	CGCGCGCGCG	GGAATATCCG	GTCCATGCCCT	120
AGCCCCGCGA	CGGCGAGCGC	CGGAATCGCG	CGAGTGAGGA	GGCGGGCAAT	TTGCGGCGGC	180
CGCGCGACCG	CGAGCGCGCG	AATGCGCGCA	GTGAGGAGGC	GGGCAATCAT	GCCAGCGCTG	240
ATCCAATCAA	CCTGCAATCG	GCCTGCGGGC	CCATTTGACA	ATCGAGGTAG	TGAGCGCAAA	300

TGATGATGG AAAACGGGCG GTGACGTCCG CTGTTCTGGT GGTGCTAGGT GCCTGCCCTGG	360
CCTTGTGGCT ATCAGGATGT TCTTCCCGGA AACCTGATGC CGAGGAACAG GGTGTTCCCG	420
TGAGCCCGAC GGGTCCGAC CCCGCCCTCC TCCCGAGAT CAGGCACTCC CTGATCCGA	480
CRAAGGGTT GACCAAGCTG CACGTAGCGG TCCGAACAAC CCGGAAAGTC GACAGCTTGC	540
TGGGTATTAC CAGTGCCTGT GTGACGTCCG GGGCCATCC GCTCCCGGCA AAGGGCGTAT	600
GCACCTACAA CGACGAGCAG GGTGTCCCTT TTGGGTACA AGGCGACAAC ATCTCGGTGA	660
AATGTTTGA CAGTGGAGC AATCTCGCT CGATTCTGA ACTGTCAACT TCACGCTGC	720
TCGATCCTGC CGCTGGGCTG ACGCAGCTGC TGTCCGGTGT CACGACCTC CAAGCGAAG	780
GTACCGAAGT GATAGACGA ATTTGACCA CCATAATCAG CCGGACCATC CCCCGAGCT	840
CTGTCAAGAT GCTTGATCCT GCGGCCAGAG GTGCAAGGCC GCGGACCTG TGGATTGCCC	900
AGGACGCTC GCACACCTC GTCCGAGCGA GCATCGACT CGGATCCGG TCGATTGAGC	960
TCACGCACTC GAAATGGAAC GAACCGCTCA ACGTCGACTA GCGCGAAGTT GCGTCGAGC	1020
GTTGNTCGAA ACGCCCTTGT GAACGCTGTC AACGGNAC	1058

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATTCCGCA CGAGAGGTGA TCGACATCAT CCGGACCAGC CCCACATCCT GGGACAGGC	60
GGCGGCGGAG GCGGTCCAGC GCGCGCGGGA TAGGCTCAT GACATCCGGG TGGTCCGGT	120
CATTGAGCAG GACATGGCCG TGGACAGGCG CGGCAAGATC ACCTACCGCA TCAAGCTCGA	180
AGTGTGCTTC AAGATGAGGC CGGCGCAACC GCGCTAGCAC GGGCGGCGCA GCAAGACGCA	240
AAATCGCAGG GTTTCGGTT GATTCTGCG ATTTTGTGTC TGCTGGCGGA GGCTTACCAG	300
GCGCGGCGCA GATCCGCGTG CTGCCATATC CAGGCTGCA TCGCGATTCC GCGCGCCAGC	360
CCGAGATTAA TGCTTCGGT CAGCCCGAAC TGGCGATCC GCGGNGAGC TGATGATGA	420
CGTGGCCAG CCCGTCCATG CCGGAGTTGC CCGAGGAAAC GTGCTGCCAG GCGGGTAGGA	480
AGGTTCCGTA GCGGCGGGTG CTGACCGGCT CTGCTTACGC CCTCAGTGG GCGAGCGAGC	540
GG	542

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 913 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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CGGTGCGCGC CGCGCCTCG TTGCCCCCAT TGCCGCGGTC GCGGATCAGC TCGGCATCGC      60
CACCATCACC GCCTTTGCGG CCGGCACCGC CGGTGCGGCG GGGGCGGCGG ATGCCACCGC      120
TTGACCTTGG CGCGCGCGCG CCGCATTTGC ATACAGCACC CCGCGGGGGG CACCGTTACC      180
GCGGTGCGCA CGGTGCGCGC CGGTGCGGTT TCAGCGCGCG GAGCGCGAAT GAACGCGCGC      240
CAAGCGCGCG CGCGGCACCG TTGCGGCTTT TTCCGCGCGC CGCGCGGCGC CGCGCAATTG      300
CGGAACAGCG AMGCACCGTT GCGCGCAGCG CCGCGCGCGT TAACGCGCGT GCGCGGCGCG      360
GCGGCGCGAC CGCGCATTTAC CGCGGTTGCG GTTCGCGTGC CCGCGGTTAC CGCGCGCGCG      420
GTTTGC CGCG AATATTCGCG GCGCACCGCG AGACCGCGCG GCGCGACCAT TGCGCGCGCG      480
CACCGAACA ACAGCGCGAG GTGCGCGCG GCGCGCGCGT TTGCGCGCAT CACCGGCGAT      540
TCACCGCGAG CACCGCGGTT AATGTTTATG AAGCGCGTAC CGCGAGCGCG GCGCGTATTG      600
CGCGCGCGCG GAGGCGCGTC CCGCGCGCGC CGCGACCGCG CAAAGCGCGG GCGTTGCGAC      660
CGCGCGCGCG GAGCGCGAGG GTGCGCGCGA TCCTCGCGTT GCGCGCGGTC CCGCGCGCAT      720
TGGTGTGCTT GAAGCGGTTA GCGCGCGTTC CGCGGTTTCC GCGCGTGGCG CCGTGGCGCG      780
CGCGCGCGCG GTTGCCTTAC AGCGACCGCG CCGTGGCGCT GTTGC CGCGA TTGCGCGCAT      840
TGCGCGCGTT GCGCGCATTG CCGCGGTTCC CGCGCGCACC GCGCGGTTGG CCGCGCGCGC      900
CGCGCGCGCG CGC

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1872 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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GACTACGTTG GTGTAGAAAA ATCTGCGCGC CCGGACCGTT AAGCGTGGGA CAATTTCTGA      60
TAGCTACCGC GACACAGGAG GTTACGGGAT GAGCAATTGG CCGCGCGCGT CACTCAGGTC      120

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GTGATGGTTG CTGAGCGTGC TGGCTGCCGT CCGGCTGGGC CTGSCCAGCG CGCCGSCCCG	180
GGCGSCCCCG CCGCCCTTGT CGCAGGACCG GTTCGCGGAC TTCCCCGCGC TGCCCTCTCA	240
CCGCTGCGCG ATGGTCGCGC AAGTGGCGCC ACAGGTGGTC AACATCAACA CCAAACTGGG	300
CTACAACAAC GCGGTGGGCG CCGGGACCGG CATCGTCATC GATCCCAACG GTGTGGTGCT	360
GACCAACAAC CACGTGATCG CCGGCGCCAC CGACATCAAT GCCTTCAGCG TCGGCTCCGG	420
CCAAACCTAC GCGGTGATG TGGTCGGGTA TGACCCGACC CAGGATGTGG CGGTGCTGCA	480
GCTGCGCGGT GCGGCTGGCG TGGGCTGGC GCGGATCGGT GCGGCGCTCG CGGTGGTGCA	540
GCGGCTGGTC GCGATGGGCA ACAGCGGTGG GCAGGGCGGA ACCCGCGCTG CGGTGGCTGG	600
CAGGTTGGTC GCGCTCGGCG AAACCGTGCA GCGCTCGCAT TCGCTGAGCG GTGCGGAGCA	660
GACATTAAC GGGTTGATCG AGTTGATCG CGCATCCAG CCGGTTGATG CCGGCGGGCG	720
CGTGTGACG GCGCTAGGAC AGGTGGTGGG TATGACACCG GCGCGCTCG ATAACTTCCA	780
GCTGTGCGAG GGTGGGCGG GATTGCGCAT TCGGATCGGG CAGGCGATGG CGATCGCGGG	840
CCAAATCGCA TCGGCTGGGG GTTACCCAC GTTTCATATC GGGGCTACCG GTTTCCTCGG	900
CTTGGGTGTT GTGACACAAC ACGGCAACCG CGACCGATC CAACGCGTGG TCGGAAGCGC	960
TGGGGCGGCA AGTCTCGGCA TCTCCACCGG CGACGTCATC ACCGCGGTGG ACCGGCGTCC	1020
GATCAACTCG GCGACCGCGA TGGCGGACGC GCTTAACGGG CATCATCCCG GTGACGTCAT	1080
CTCGGTGAAC TGGCAAAACA AGTGGGGCGG CAGCGGTACA GGGAACTGCA CATTTGCCGA	1140
GGGACCCCGG GCGTGATTC TCGGGATAC CACCGCGCGG CCGGCGAATT GCGTTGGCGC	1200
CAGCGTAT TCGCGGTGCA GCGCGGAGT TCGCTCTCC GTGCGCGTGG CATTTGGGAA	1260
GCAATGAACG AGGCAGAAC CAGCGTTGAG CACCGTCCCG TCGAGGGCAG TTACGTGGA	1320
GGCGGTGTGG TCGAGCATCC GCGTCCAG GACTTCGGCA GCGCGCGCGC CTTGCGCGCG	1380
GATCGGACCT GGTTAAGCA GCGCGTCTC TACGAGGTGC TGGTCCGGCC GTTCTTCSAC	1440
GCGAGCGCGG ACGGTTCCG GCGTCTGCGT GCGCTCATCG ATCGCGTCA CTACCTGCG	1500
TGGGTTGGCA TCGACTGCAT CTGTTGCGCG GCTTCTACG ACTCACCGGT GCGGAGCGC	1560
GCTTACGACA TTGCGGACTT CTACAAGGTG CTGCGCGAAT TCGGACCGGT CGACGATTC	1620
GTGCGCTTGG TCGACACGCG TCGCGGCGA GGTATCCGCA TCGTACCGCA CTTGGTGGT	1680
AATCACACCT CCGAGTCCCA CCGCTGGTTT CAGGAGTCCC GCGCGGACCG AGACGAGCG	1740
TACGGTGAAT ATTACTGTG GAGCGACACC AGCGAGCGCT ACACCGAGCG CCGGATCAAT	1800
TTGCTGACA CCGAGAGTGC GAACTGGTCA TTGATCTCG TCGCGGACA GTTCTACTG	1860
GCACTGATTC TT	1872

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1492 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCGCCGAA ACCTGATGCC GAGGAACAGG GTTTCCTCCGT GAGCCCGACG GCGTCCGACC	60
CCGCGCTCCT CCGCGAGATC AGGCAGTCGC TTGATCGGAC AAAAGGCTTC ACCAGCGTGC	120
ACGTAGCGGT CCGAACAACC GGGAAAGTCG ACAGCTTGCT GGGTATTACC AGTGGCGATG	180
TCGACGTCCG GGCCAATCCG CTCGCGGCCAA AGGCGGTATG CAGCTACAAC GACGAGCAGG	240
GTGTCCCGTT TCGGCTACAA GCGGACABCA TCTCGGTGAA ACTGTTCCGAC GACTGGAGCA	300
ATCTCGGCTC GATTTCGAA CTGTCAACTT CAGCGTGTCT CGATCTTCCC GCTGGGGTGA	360
CCGAGCTGCT GTCCGCTGTG ACCAAGCTTC AAGCGCAAGG TACCGAAGTG ATAGACGGAA	420
TTTCGACCAC CAAAATCACC GGGACCATCC CCGCGAGCTC TGTCAAGATG CTTGATCCTG	480
GGCCCAAGAG TGCAAGGCCG GCGACCTGTG GGATTGCCA GCGCGGCTCG CACCACTCTG	540
TCCGAGCGAG CATCGACCTC GGATCCGGGT CGATTCACTT CACGCACTCG AAATGGAAAG	600
AACCGGTCAA CGTCGACTAG GCGGAAGTTG CCGCGACGCG TTGCTCGAAA CGCCCTTGTC	660
AACGCTGTCA ACCGCACCCG AAAACTGACC CCTGACGGC ATCTGAAAT TGACCCCCTA	720
GACCGGGCGG TTGCTGCTTA TTCTTCGGTG GTTCCGGCTG GTGGGACGGG GCGGAGGTGG	780
CGGTCTTTGA GCGGTAGCT GTGCGCTTTG AGGGGAGCGA CTTGAGCATG GTGGACGAGG	840
CGGTGATCA TGGCGGCAGC AACGACGTGG TCGCGGCCGA AAACCTGCCC CCACCGGCGG	900
AAGGCTTAT TGGACGTGAC GATCAGCTG GCGGCTCAT ACCGGGAGGA CACCACTGG	960
AAGAAGAGCT TGGCGGCTC GGGCTCAAAC GGAATGTATC CGACTTCCTC AACTACCAGG	1020
AGCGGATAAC GGGCAAACCG GGTGAGTTCC GCGTAGATCC GCGCGGGGTG GTGAGCCTCG	1080
GCGAACCGTG CTACCCATTC GCGCGGCGTG GCGAACAGCA CCGGATGACC GGCTTGACAC	1140
GCGGCTATCG CCAGGCGCAC GCGAGATGA GTCTTCCCGG TGCCAGGCGG GCGCCAAAAA	1200
CACGAGGTTA TCGCGGGCGG TGATGAAATC CAGGCTGCCC AGATGTGCGA TGCTGTGCGG	1260
TTTGAGGCCA CGAGCATGCT CAAAGTCGAA CTCTTCCAAC GACTTCCGAA CCGGGAAGCG	1320
GGCGGCGCGG ATCGGGGCT CAGGACCATG GCACTCCCGG GTTGACACTT CCGGCTGCAG	1380
GCAGGCGGCG AGGTATTCTT CGTGGCTCCA GTTCTCGGCG CAGGCGCGAT CCGCCAGCCG	1440
GGACACTGAC TCACGCAGGG TGGGAGCTTT CAATGCTCTT GT	1492

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 876 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

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GAATTCGGCA CGAGCCGGGG ATAGCTTCTG GGCGCGGGCC GACCAGATGG CTCGAGGGTT      60
CGTGTCTGGG GCCACGGGGG GCGGCACCCAC CCGGACGGGT GAGGGGCTGC AACAGGCGGA      120
CGGTCACTCG TTGCTGCTGG ACCGCCACCA CCCGGGGGTG GTTGCTTACC ACCCGGCTTT      180
CGGCTACGAA ATCGGCTACA TCGGGGAAG CGGACTGGCC AGGATGTGG GCGAGAACCC      240
GGAGAACATC TTCTTCTACA TCACCGTCTA CAACGAGCCG TACGTGCAGC CGCGGGAGCC      300
GGAGAACTTC GATCCCGAGG GCGTCTGGG GGGTATCTAC CCGTATCAG CGGCCACCGA      360
GCAACGCACC AACAAGGNGC AGATCCTGGC CTCGGGGTA GCGATGCCC CGGCGCTGGC      420
GGCAGCACAG ATGCTGGCGG CGGAGTGGGA TGTGCGGGC GACGTGTGGT CGGTGACCAG      480
TTGGGGCGAG CTAARCCGCG ACGGGGTGGT CATCGAGACC GAGAAGCTCC GGCACCCGCA      540
TCGGCCGGCG GCGGTGCGCT ACGTGACGAG AGCGCTGGAG AATGCTCGGG GCGCGGTGAT      600
CGCGGTGTGG GACTGGATGC GCGCGGTCCC CGAGCAGATC CGACCGTGGG TCGCGGGCAC      660
ATACCTTACG TTGGGCACCG ACGGTTTGGG TTTTTCGGAC ACTGGGXXX CGGTCGTTCG      720
TTACTTCAAC ACGAGCGCG AATCCAGGT TGGTCGGGT TTTGGGAGCG GTTGGCCCGG      780
TCGACGGGTG AATATCGACC CATTGGGTGC CGGTCTGGG CCGCCCGCCC AGTTACCCGG      840
ATTCGACCAA GGTGGGGGGT TCGCCCCGAN TAGTT      876

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(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1021 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

ATCCCCCGG GGTGCAGAA TTCGGCAGCA GAGACAAAAT TCCAGCGCTT AATGCAGGAA      60
CAGATTCATA ACGAATTCAC AGCGGCACAA CAATATGTTC CGATCGCGGT TTATTTGAC      120

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ACCGAAGACC TCCCGCASTT GCGGAGCAT TTTTACAGCC AAGCGCTCGA GGAACGAAAC 180
CATGCAATGA TGCTGTGCA ACACCTGCTC GACCGCGACC TTCGTGTGCA AATTCCTGGC 240
GTAGACACGG TCGGAAACCA GTTCGACAGA CCCCCTGAGG CACTGCGGCT GCGGCTCGAT 300
CAGGAACGCA CAGTCACCGA CCAGGTCGCT CCGCTGACAG CGGTGCCCCG CGACGAGGGC 360
GATTTOCTCG GCGACAGTT CAGGAGTGG TTCTTGACAG AACAGATGCA AGAGGTGGCC 420
TTGATGGCAA CCTGTGTGCG GGTTCGGAT CCGGCGGGG CCAACCTGTT CGAGCTAGAG 480
AATTCTGTG CAGCTGAAGT GATGTGGCG CCGCCGCTAT CAGCGCGCCC GACGCTTCCC 540
GGGGCGCGCC TCTAGATCCC TGGGGGGCAT CAGCGAGTGG TCCCGTTCGC CCGCGCTCT 600
TCCAGCCAGG CTTTGTGCG GCGGGGTG TGAGTACCA TCCAGGCCAC CCGGACCTCC 660
CGGAAAAAGT CGATGTCTC GTACTCATCG ACGTTCCAGG AGTACACCGC CCGGCTTGA 720
GCTGCGGAGC GGTCAACGAG TTCCGATAT TCCTTTAAGC CAGGCACTGA GGTGCCACC 780
GCGGTTGGCC CGACCGGCT GCGGCACTG CTGCTCAGG ATCGGGGGGT CTGCGGAGC 840
AACAAAGTGG GCAGGAGGGG TGGAGCCCGC CGGATCCCA GACCGGGGG GCGAAACGA 900
CATCAACACC GCACGGGATC GATCTGCGA GGGGGTGGC GGAATACCA ACCGCTTAG 960
GAGCGCCAGC ACTTGTTTT CCACCAGCA AGGCTTTTGG GGTCACTGGN GCGNNTAAG 1020
T 1021

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(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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CTGCGGACG AACGGAAGAA CACAACCATG AAGATGGTGA AATCGATCGC GCGAGTCTG 60
ACCGCCGCGG CTGCAATCGG CCGCGCTGCG GCGGTGTGA CTTGATCAT GGTGGCGGN 120
CGGTCGTAT ACCAGATGCA GTCGTCGTC TTCGCGGCG CACTGCGGCT GCGGCGGNA 180
TGGCGGCTG AGTCCCCGAC CCGCGCCGAG TGGACGAGC TGCTCAACAG NCTGCGCAT 240
CCCAACGTGT CGTTTNGAA CAGGCGAGT CTGCTGAGG GNGGNATCG NCGNACGAG 300
GNGNAGATC GNGAGACAA A 321

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCCTATCGGT TCCGCTTGGC GACGGGTTTT GCGNCCGGGT GGTAAACCGG CTCGGCCAGC	60
CGATCGACGG GCGCGGAGAC GTCGACTCCG ATACTCGGCG CCGCTGGAG CTCAGGCGC	120
CCTCGGTGGT GNACCGGCAA GCGGTGAAGG AGCCCTTGA GACCGGATC AAGGCGATG	180
ACGCEATGAC CCGCATCGGC CGCGGGCAGC GCGACTGAT CAYCGGGAG CCGAGAGCG	240
GC AAAAACCG CGCTCTGTGT CGGACACCAT CCTCAAAUCA GCGGGAAGAA CTGGGASTCC	300
GGTGGATCCG AAGAAGCAGG TCGCTTGTG TATACGTTG CCATCGGGCA AGAAGGGGAA	360
CTTACCATCG CCG	373

(2) INFORMATION FOR SEQ ID NO:23:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGAGCCGCT GATGGGATTC CTGGGCGGGG CCGGTCCGCT GCGGGTGGTG GATCAGCAAC	60
TGGTACCCG GGTGCCGCAA GCGTGGTCCT TTGCTCAGGC AGCGCTGTG CCGGTGGTGT	120
TCTTGACGGC CTGGTACGGG TTGGCCGATT TAGCCGAGAT CAAGGCGGGC GAATCGGTGC	180
TGATCCATGC CGGTACCGGC GGTGTGGGCA TGCGGGCTGT GCAGCTGGCT CGCCAGTGGC	240
GCGTGGAGGT TTTCGTCAAC GCCAGCCGTG GNAAGTCGA CACCGTGGC GCGATNGNST	300
TTGACGACGA GCCATATCGG NGATTCCGNC ACATNGAAG TTCCGANGGA GA	352

(2) INFORMATION FOR SEQ ID NO:24:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

{x1} SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCCSCG	FTCATTCGGT	TCGACGAGCG	GCTGGCGATA	ATCGACGAAG	TGATCAAGCC	60
GCGGTTCCCG	GCGCTCATGG	GTACACGCGA	GTAATCAGCA	ACTTCTCTGG	TATATCCGAC	120
CTAGCGTCCA	GTTGCTTSCG	AGATCGCTTT	CGTACCGTCA	TGGCATGTAC	CGGTTGCGGT	180
GCGGACGCGT	CAAGCTGGCG	GCGTGCATCC	TGGCCACGGG	TGTGGCGGGT	CTCGGGGTCG	240
GCGGCGAGTC	CGCAGCCCAA	ACCGGCGCCG	TGCCCCACTA	CTACTGGTGC	CCGGGGCAGC	300
CTTTCGACCC	CGCATGGGGG	CCCACTGGG	ATCCCTACAC	CTGCCATGAC	GACTTCCACC	360
GCGACAGCGA	CGGCCCCGAC	CACAGCCGCG	ACTACCCCGG	ACCCATCCTC	GAAGGTCCCG	420
TGCTTGACGA	TCCCGGTGCT	GCGCCGCGCG	CCCCGCTGC	CGGTGGCGGC	GCAATGCGCT	480
CGTTGACCGG	GCGGCATCAG	CGAATACGGG	TATAAACCCG	GGGTGGCCCC	CGGCAAGCTA	540
CGACCCCCCG	CGGGGCAGAT	TTACGCTCCC	GTGGCGATGG	ATCGCGCGGT	CGGATGACAG	600
AAAATAGSCG	ACGGTTTTGG	CAACCGCTTG	GAGGAGGCTT	GAAGGGAACC	TGTCATGAC	660
GCGGACAGCG	CCTCCACCAT	CGACATCGAC	AAGGTTGTTA	CCCGCACACG	CGTTGCGCGG	720
ATCGTG						726

{2} INFORMATION FOR SEQ ID NO:25:

{i} SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

{x1} SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGACGACC	ACGAACGTGG	GGCCCAACAC	CGCCTATGCG	TTGATGCGAG	CGACCGGGAT	60
GGTCGCGGAC	CATATCCAAG	CATGCTGGGT	GCTCACTGAG	CGACCTTTTG	ACCAGCCCGG	120
CTGCCCCGATG	GCGGCCCCGT	GAAGTCATTG	CGCCGCGGCT	TGTGCACCTG	ATGAACCGCA	180
ATAGCGAACA	ATAGGGGGGT	GATTTGGCAG	TTCAATGTGG	GGTATGGCTG	GAAATCCAAT	240
GCGCGGGCAT	GCTCGGCGCC	GACCAAGGTC	GCGCAGGCGG	GCCAGCCCGA	ATCTGAGGGG	300
AGCACTCAAT	GGCGGCGATG	AAGCCCCGGA	CGGCGACGGG	TCCTTTGGAA	GCACTAAGG	360
AGGGGCGCGG	CATTGTGATG	CGASTACCAC	TTGAGGCTGG	CGGTGCGCTG	GTCGTGAGGC	420
TGACACCCGA	CGAAGCCGCG	GCACTGGGTG	ACGAACTCAA	AGGCCTTACT	AGCTAAGACC	480
AGCCCCAAGG	CGAATGCTGG	GCGTTACGGG	CACACCTTCC	GGTAGATGTC	CAGTGTCTGC	540
TGCGCGATGT	ATGCCGAGGA	GAACTCTTGG	ATACAGCCTT			580

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

AACGGAGCGC CCGGGGTTTT TGGCGGGGCC GGGCGGTCG GGGGCAACG CCGGGCCGGC      60
GGTACCGCCG GGTGTTCG TGTCCGCGGG GCGGTGGCG CCGGAGGCAA CCGCATCGCC      120
GGTGTACCGG GTACGTGGG CAGCACACCG GTTGATCCG                                160

```

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

GACACCGATA CGATGGTGT GTACGCCAAC GTTGTGACA CGCTCGAGGC GTTCACGATC      60
CAGCGCACAC CCGACGGCGT GACCATGGCG GATGGGGCC CTTGCGCGA GCGCGCTGCG      120
AAGCGGATGG GAATCGACAA GCTGCGGGTA ATTATACCG GAATGGACCC GTTCGTGGGT      180
GAACCGGAC AGTGGGACGA CCGCAACAAC ACCTTGGCGT TGGCGCCCGG TGTGTTGTC      240
GGCTACGAGC CCAACGTACA GACCAACGCG CG                                272

```

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 317 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

GCAGCCGGTG GTTCTCGAC TATCTGCGCA CGGTGACGCA GCGGACGTC CCGAGCTGA      60
AGCGGATCGA GCAGACGAT CGCCTGCCGC GGTTCATGCG CTACCTGGCC GCTATCACC      120

```

```

CGCAGGAGCT GAACTGGCC GAGCGGGCG GGTTCATCGG GGTGACCGG GGCACCATCC 100
GTTGCGATCT GGGTGGTTC GAGACGGTCT ATCTGGTACA TGCGCTGCC GCTTGGTCC 240
GGATCTGAC CGCGAAGATC AAGAAGCGT CAAAGATCCA CCGCTCGAC AGTGGCTTCG 300
CGCCCTGCTT GCGGGG 317

```

(2) INFORMATION FOR SEQ ID NO:29:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

GATCGTGGAG CTGTCGATGA ACAGCCTTGC CGGACGCGC GCGGCCAGCA CGTCGCTGA 60
GCAGCGCCCG ACCACCTCGC CGTGGGCGAG CATGGTGATG ACCACGTCGG CCTCGGCCAC 120
CGCTTCGGCG CGGCTACGAA ACACCGCGAC ACCGTGCGCG GCGGCGCCCG ACCCGCCGT 180
GC 192

```

(2) INFORMATION FOR SEQ ID NO:30:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

GATCGCGAAG TTTGGTCAAC AGGTGGTCTG CGCGAAAGTC TGGGCGCTCT CGAAGCGGGT 60
CGGCGTTCAC GAGGCGAAGA CACCGCTGTC CGAGCTGCTC CGGCTGCTCT ACCGCGGCA 120
GAGGTTGAGA TTGCCCCCG CGCGAGCGCG GTAGCAAGAC TTGTGCGCTT GATCCTCAT 180
GAGACTCGGC GGTTAGCCAT TGACCATGGC GTGTACCGCG TGCCCGAGCA TTTGACGCT 240
CCGTTGTCAG ACCACGTGCT CGAACGCTTT CACCGGTGAA GCGCTACCTC ATCGACACCC 300
ACGTTTGG 308

```

(2) INFORMATION FOR SEQ ID NO:31:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGACGACGA GCAACTCAGG TGGATGATGG TGGCAGCGG CATTGAGGAC GGAGAGAATC	60
CGGCCGAAGC TSCCGCGCGG CAACTGCTCA TAGTGACCGG CCGTAGAGGG CTCCCCCGAT	120
GGCACCGGAC TATTCTGGTG TCCCGCTGGC CCGTAAGAGC GGCTNAAAGA ATGTGAGGGG	180
ACACGATGAG CAATCACACC TACCGAGTGA TCGAGATGGT CCGGACCTCG CCGGACGGCG	240
TGACCGCGGC AATCCAGGGC GGTCTGG	267

(2) INFORMATION FOR SEQ ID NO:32:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1539 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCGTSCCGA AAGAATGTGA GGGGACACGA TGAGCAATCA CACCTACCGA GTGATCGAGA	60
TGCTCGGGAC CTGCGCCGAC GCGGTGAGCG CCGCAATCCA GGGCGGTCTG GCCCGAGCTG	120
CGGAGACCAT GCGCGCGCTG GACTGGTTGG AGTACAGTC AATTGAGGGC CACCTGGTGG	180
ACGGAGCGGT GCGGCACTTC CAGGTGACTA TGAAAGTCGG CTTCGGCTGG AGGATTCCTG	240
AACCTTCBAG CCGGCGGAT AACTGAGGTG CATCATTAAG CGACTTTTCC AGAACATCCT	300
GAGCGCTCG AAACCGGGTT CAGCGGACGG TGGCTCCGCC GAGGCGCTGC CTCCAAAATC	360
CCTGCGACAA TTCTCGGGCG GCGGCTACAA GGAAGTGGT GCTGAATTGG TCGGGTATCT	420
GGTCGACCTG TGTGGGCTGC AGCGGGACGA AGCGGTGCTC GACGTGCGCT GCGGCTCGGG	480
GCGGATGGCG TTGCGGCTCA CCGGCTATCT GACAGCGAG GAGCGCTACG CCGGCTTCCA	540
TATCTGCGAG AAAGCCATCG CGTGGTGCCA GGAGCACATC ACCTCGGGCG ACGCCAACTT	600
CCAGTTGAGG GTCTCCGACA TGTACAATTC GCTGTACAAC CCGAAAGGGA AATACCACTC	660
ACTAGACTTT CGCTTTCCAT ATCGGATGTC GTGTTTGGAT GTGGTGTTC TTACCTCGGT	720
GTTACCCAC ATGTTTCCGC CCGAGTTGGA GCGTATCTG GAGGAGATCT CCGCGTGTCT	780
GAAGCCCGGC GGACGATGCC TGTGCACSTA CTCTTGTCT AATGACGAGT CATTAGCCCA	840
CATCGCGGAA GGAAGAGTGG CGCACTACTT CCAGCATGAG GGACCGGCTT ATCGGACAT	900

CCACACAGAG	CGGCCCCGAG	AAGCAATCGG	CTTGCCGGAG	ACCTTCCTCA	GGGATGCTCA	980
TGGCAAGTTC	GGGCTCGCCG	TGCACGAACC	ATTGCACTAC	GGCTCATGCA	GTGGCCGSCA	1020
ACCACGCCTA	AGCTTCCAGG	ACATCGTCAT	CGGACCAAA	ACCGCGAGCT	AGGTCCGCAT	1060
CCGGGAAGCA	TGCGACACC	GTGGCGCCGA	GGGCGCTGC	CGGCAGGCCG	ATTAGGCGCG	1140
CAGATTASCC	CGCCCGGCT	CCCGGCTCCG	AGTACGGGCG	CCCGAATGGC	GTCACCGGCT	1200
GGTAACCACG	CTTGCCGCC	TGGGCGGCGG	CCTGCGGAT	CAGGTGGTAG	ATGCCGACAA	1260
AGCCTGCSTG	ATCGGTCATC	ACCAACGGTG	ACAGCAGCCG	GTGTGTCACC	AGCGCGAACC	1320
CCACCCCGGT	CTCCGGTCT	GTCCAGCCGA	TGAGCCGCC	CAAGCCGACA	TGACCAAAAC	1380
CCGGCATCAC	GTTGCGGATC	GGCATACCGT	GATAGCCGAG	ATGAAAATTT	AAGGCGACCA	1440
ATAGATTTGG	ATCCGGCAGA	ACTTGCCTTC	GGTTGCGGCT	CAGGCCCGTG	ACCAGCTCCC	1500
GCGACAAGAA	CCGTATGCCG	TGATCTCCG	CTCGTGCCG			1539

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 851 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGCGTG	CGGTGATGA	GCCTCAGCCG	GGGCGAGGCC	GAGCTGACCG	CGGCCCAGCT	60
CCGGATTGCT	CGGGCGGCGT	ACGAGACGGC	GATGCGGCTG	ACGGTGCCCC	CGCCCGTGAT	120
CGCCGAGAAC	CGTCTGAAC	TGATGATTCT	GATAGCGACC	AACCTCTTGG	GCCAAAACAC	180
CCCGGCGATC	CGGTCAAGG	AGCCGGAATA	CGGCGAGATG	TGGGCCCCAAG	ACGCGCGCGC	240
GATGTTTGGC	TACGCCGCGG	CGACGGCGAC	GGCGACGGCG	ACGTTGCTGC	CGTTGAGGCA	300
GGCGCGGGAG	ATGACCAGCG	CGGTGGGCT	CCTCGAGCAG	GGCGCGCGCG	TGAGGAGGCG	360
CTCCGACACC	GGCGCGGCGA	ACGAGTTGAT	GAACATGTG	CCCGAGGCGC	TGAAACAGTT	420
GGCCAGGCC	ACGAGGCGCA	CCAGCCCTTC	TTCAGGCTG	GGTGGCTGT	CGAGACGGT	480
CTCGCCGCAT	CGGTGCGCGA	TCAGCAACAT	GGTGTGATG	GCCAACCAAC	ACGTGTGAT	540
GACCAACTCG	GGTGTGTGGA	TAACCAACAC	CTTACGCTCG	ATGTTGAAGG	GCTTGTCTCC	600
GGCGCGGGGC	GGCAGGCGCG	TGCAACCTGC	GGCGCAAAAC	GGGCTCCCGG	CGATGAGCTC	660
GCTGGGCAGC	TGGCTGGGTT	CTTGGGCTCT	GGCGGCTGGG	GTGGCGGCGA	ACTTGGGTCG	720
GGCGGCTCG	GTACGCTATG	GTCACCGGGA	TGGCGGAAAA	TATGCAAGAT	CTGGTCCGCG	780

GAAAGGTCGT CCGCCGTAAG GTTTACCCCC GTTTTCTGGA TGGGCTGAAC TTGCTCAGCG 840
GAAACAGTTA C 851

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCGATCGG CCGGAAATTT GGACCAGATT CCGCTCCGGC GATAACECAA TCAATCGAAC 60
CTAGATTTAT TCGCTCCAGG GGGCCGAGTA ATGGCTCCCA GGAGAGGAAC CTTACTGCTG 120
CGGSCACTG TCGTAGSTCC TCGATACGGC GCGAGGCTC GACATTTTCC ACCGACACCC 180
CCATCCAAAC GTTCGAGGGC CACTCCAGCT TGTGAGCGAG GCGAGCGCAAT CGCAGGCTGC 240
GCTTGGTCAA GATC 254

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCTTGACC GAAGCGGCCG CCGCCAGGC GAAGTCGTC TTGGACCAGG AGGGACGGGA 60
CGATCTGGCG CTGCGGATCG CGGTTCAAGC GGGGGGGTGC GCTGGATTGC GCTATAACCT 120
TTTCTTCGAC GACCGGACGC TGGATGGTGA CCAAAACCGC GAGTTCGCTC GTGTCAGATT 180
GATCTGGAC CGGATGAGCG CCGCGTATGT GGAAGCGCGC TCGATCGATT TCGTCGACAC 240
TATTGAGAA GCAAGGTTAC CAGTCAAAAT CCGACGCGCA CCGGCTCCTG CCGCTGCGGG 300
GATTCGTTCA ACTGATAAAA CGCTAGTACG ACCCGGCGGT GCGCAACACG TACGAGCACA 360
CCAAGACCTG ACCGCGCTGG AAAAGCAACT GAGCGATGCC TTGCACCTGA CCGGCTGGCG 420
GGCGCGCGCG GGCAGGTGTC ACCTGCATGG TGAACAGCAC CTGGGCTGGA TATTGCGGCC 480
AGTACACGAT TTTGTGATC GAGGTCACCT CGACCTGGCA GAACTGCTTG CCGAAGCCGT 540
CGCTGCTCAG CTTGGCCAG GCGTGATCGG AGCGCTGTC GCGCAGCGCG TCGTGGATAC 600

```

CCCACAGCCG ATTCCGAACG ATGCTGTCCA CATCCCGCTT CTCACGCGCG TTGAGGTATC      660
CCTGAATCGC GGTTTTGGCC GGTCCCTCCG AGAATGTSCC TGCCGTGTTC GCTCCGTTCG      720
TGCCGACCCC GATATGATC GCGCGCGTCA TAGCCGACAC CAGCGCGAGG GCTACCACAA      780
TGCCGATCAG CAGCCGCTTC TGCCGTCCCT TCGGCTAGGA CACCTGCGGC GGCACGCCCG      840
GATATCCCGC GGGCGGCGAG GCGCGCTCCT CTGCCCGTCC CGGCGCGAGC GCGCGTTCCG      900
CGGCGCGCAG GTCGTGGGGG TACTCCAGGG CTTCGGCTTC GTGGGATGAG GGCTCGGGGT      960
ACGCGCGCGG TCGTTGGTG CCGACACCGG GGTTCGGCGA GTGGGACCG GGCATTGTGG     1020
TTCTCCTAGG GTGGTGGAGG GGACCAGCTG CTAGGGCGAC AACCGCCCGT CGGCTCAGCC     1080
GGCAGCATCG GCAATCAGGT GAGCTCCCTA GGCAGGCTAG CGCAACAGCT GCGTTCAGCT     1140
CTCAACSCGA CGGGCGGGC CGCGCGCGCG ATAATGTTGA AAGACTAGGC AACTTAGGA     1200
ACCAAGGAGC GAGATTTTGT GACGATC                                     1227

```

(2) INFORMATION FOR SEQ ID NO:36:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 181 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

GGGTGTCCG CGGATCCGC GGTGCTTGA ACCGCAACCG CGGGCCCGC GGGCGGCG      60
GGACCGCCCC TAACGGTGGT GCGCGCGCA AGCCTGCTT GTTCGGGCG GCGCGCTCCG     120
GCGGCGCGC CACCAATGCT GGTGCGCG GGTCCGCGG ATTTGCTAC GGCACCGCG      180
G                                                    181

```

(2) INFORMATION FOR SEQ ID NO:37:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

GCGTGTCCG CGGATCCGC GGTGCTTGA ACCGCAACCG CGGTGTCCG GCGCGGCG      60
GGACCGCGCT CTTGCGGCT GCGCGCGCC AGGCGCGCT CCGTGGGCG GCGCGCAATG     120

```

```

GGGGGGGGCTC CACCCGCGGC AACGGCGGTC TTGGCGGCGC GGGGCGTGCC GGAGGCAACG      180
CCCCGGACCG CGGCTTCGGT GGCAACGGCG GTAAGGGTGG CCAGGGCGGN ATTGGCGGCG      240
GCACTCAGAG CGCGACGGGC CTCGCGGTG ACGGGGCTGA CGGCGGTGAC                    290

```

(2) INFORMATION FOR SEQ ID NO:38:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

GATCCAGTGG CATGGGGGT GTCAGTGGAA GCAT                                     34

```

(2) INFORMATION FOR SEQ ID NO:39:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

GATCGCTGCT CTTCCDCCCC TTGCGCGCGA CGCCACCGGT CCCACCGTTA CCGAACAAAGC      60
TGGCGTGCTC GCGAGCACCC CCGGCACCGC CGACCGCGGA GTCGAACAAAT GGCACCGTCC      120
TATCCCCACC ATTGCGCGCG GCGCCACCGG CACCG                                155

```

(2) INFORMATION FOR SEQ ID NO:40:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

ATGGCCTTCA CCGGGCCCCG GGCACCGGCG AGCCCGGCGG GCGCGCGCGG TGG          53

```

(2) INFORMATION FOR SEQ ID NO:41:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCCACCGC GGGTGCAGAC GGTGCCCCCG GCGCCACCCC GACCAGCGGC GGCAACGGCG	60
GCACCGCGCG CAACGGCGCG AACGCCACCG TCTCGGCGG GCGCGCGCGG CCGCGCGGCA	120
AGGGCGGCAA CG	132

(2) INFORMATION FOR SEQ ID NO:42:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGGGCGC CGGACCGGC GGGGACGGCG GCAAGGGCGG NAACGGGGGC GCGGACCCA	60
CCGCGCAAGA ATCTTCGNG TCCNCCAATG GCGGCAATGG CGGACAGGGC GGCACGGCG	120
GCANCGGGCG CA	132

(2) INFORMATION FOR SEQ ID NO:43:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 702 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCAGAGG ATCGGTACCC CGCGGCATCG GCAGCTCCCG ATTCCCGCGG TTTCGCCACC	60
CGAGGAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCGCTTCG CGATGCGCGC	120
ATGAACGGGC GGCATCAAAAT TAGTCCAGGA ACCTTTCAGT TTAGCGACCA TAATGGCTAT	180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCCGAGAC CGTGACGGTG GATCAGCAAG	240
AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCGCGATGGC GGACCCACCG ACTGATGTCC	300
CCATCACACC GTGGGAATC ACCGNGGNTA AAACGCGCG CCAACAGATG GTNTTGTCCG	360

```

CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAGA GCGGCAGGCT CTGGCGACCT      420
CGCTGCGCAA CGCGGOCBAG GNGTATGGCG AGGTTGATGA GGAGGCTGGG ACCGCGCTGG      480
ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCGG GGCCTCGGA GGGACAGTT      540
CGGCGGAAC TACCGATACG CCGAGCGGTG CCACGCGCGG TGAACCCAC TTCATGATC      600
TCAAAGAAGC GCGAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTGGG      660
GGGATGGGTC GAACACTTTC ACCCTGACGC TCGAAGGCGA CG              702

```

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

GAAGCGGCAG CGCTGTGGG CGACGTGGCG GTCAAAGCGG CATCGCTCGG TGGCGGTGGA      60
GGCGGGGGGG TGCGTCCGC GCGGTTGGGA TCGCGATCG GGGGCGCCGA ATCGGTGCGG      120
CCCCGTGGCG CTGGTGACAT TGCCGGCTTA GGCCAGGGAA GGGCGGGCGG CGCGCGCGCG      180
CTGGGCGGCG GTGGCATGGG AATGCCGATG GGTGCGCGCG ATCAGGGACA AGGGGGCGCC      240
AATCCAAGG GTTCTAGCA GGAAGACGAG GCGCTCTACA CCGAGGATCC TCGTGCCG      298

```

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1058 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

CGGCACGAGG ATCGAATCGC GTGCGCGGGA GCACAGCGTC GCACTGCACC AGTGGAGGAG      60
CCATGACCTA CTGCGCGGGT AACCCCGGAT ACCCGCAAGC GCAGCCCGCA GGCTCCTACG      120
GAGCGCTCAC ACCCTCGTTC GCGGCGGCG ATGAGGGTGC GAGCAGCTA CCGATGTACC      180
TGAACATCGC GGTGGCAGTC CTCGGTCTGG CTGGGTACTT CGCACGCTC GCGCCAAATGT      240
TCAACCTCAG TACCGAAGTC GGGGGGGGTG ATGCGCGAGT GTCCGCTGAC ACTGGGCTGC      300
CGGTCGGGGT GGCTCTGCTG GCTGCGCTGC TTGCCGGGT GGTCTGCTG CCTAAGGCCA      360

```

```

AGAGCCATGT GACGCTAGTT GCGGTGCTCG GGSTACTCGG CATTATTTCTG AIGGTCTCGG      420
CGACGTTTAA CAAGCCCAAC GCCTATTCGA CCGGTGCGGC ATTGTGGGTT GTGTTGGCTT      480
TCATCGTSTT CCAGGCGGTT GCGGCAGTCC TGGCGCTCTT GGTGGAGACC GCGCCTATCA      540
CCGCGCGCGG CCGCGCGGCT AGTTGAGACC CATTATGACA GTACGGGCGG TACGGGCACT      600
ACGGGCACTA CCGGCTGACG CCGGCTGGGT ACTACGGTCA GCGGGTCTCT CAGCAGGCGG      660
CGGCACTGCA GTGCGCGCGG CCGCAGCACT CTCGCGAGCC TCCCGGATAT GGTGCGCACT      720
ACGCGCGGCTA TTCGTCCACT CCGAGCCAAT CCGGCACTCG ATACACTGCT CAGCCCCCGG      780
CCGAGCGCGG GCGGCAGTCC GGTGCGCAAC AATCGCAGCA GGGCGCATCC ACGCCACCTA      840
CCGCTTTTCC GAGCTTCAGC CCACCAACAC CGSTCACTGC CCGGACGCGG TCGCAGGCTG      900
GTTCGCTTCC ACTCAACTAT TCAAACCCCA GCGGCGCGCA GCACTGCTCG TCCCCCGGG      960
GGGCGCGGGT CTAACCGGCG GTTCCCGCGT CCGGTGCGGC GTGTGCGCGA AGATGAGCA      1020
GGGTGTCAGC AAGCGCGGAC GATCCTCGTG CCGAATTC      1088

```

(2) INFORMATION FOR SEQ ID NO:46:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(a) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

CGGCACGAGA GACCGATGCC GCTACCCCTG CCGAGGAGGC AGGTAATTTC GAGCGGATCT      60
CGGCGGACCT GAAACCCGAG ATCGACCAGG TGAGTGCAG CCGAGGTTTG TTGCAGGSCC      120
AGTGGCSCCG CCGCGCGCGG ACGGCGGCGG AGGCGCGGCT GTGCGCTTTC CAAGAGGCGG      180
CCAATAAGCA GAACGAGGAA CTCGACGAGA TCTCGACGAA TATTGCTCAG GCCGGGCTCC      240
AATACTCGAG GCGCGACGAG GAGCAGGAGC AGCGGCTGTC CTCGCAATG GCTTCTGAC      300
CCGCTAATTC GAAGAGAAAC GCAGCAA      327

```

(2) INFORMATION FOR SEQ ID NO:47:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 170 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(*1) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGCTCGCGAT	GATGGGCTTG	TGGAACGTGA	CGAATCTGT	ACCGGCGTGG	TTGAGATCAA	60
CCACACACGT	GTTGGCGTGG	GCAAATGTGG	CGACCCCGTG	GATCTCGGTG	ATCTTCTTCT	120
TCTTCATCAG	GAAGTGCACA	CCGGCCACCG	TGCGCTCGGG	TACCTTTGGG		170

(2) INFORMATION FOR SEQ ID NO:48:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(*1) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCGCGCG	CACGGGCGGT	GCGGGCGGCA	GCACCGCTGG	CGCTGGCGGC	AACGCGCGGG	60
CCGGGCGTGG	CGGCGGAACC	GGTGGGTTGG	TCTTCGCGAA	CGGCGGTGCC	GGCGGGCAGC	120
GGGCGGT						127

(2) INFORMATION FOR SEQ ID NO:49:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(*1) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGCGCGAAG	GGCGGCACCG	CGGGCAACCG	GAGCGGCGCG	GGCGGCGGCA	ACGCGCGCAA	60
CGGCGGCTCG	GGCTCAACG	G				81

(2) INFORMATION FOR SEQ ID NO:50:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(*1) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGCGT	CGCGGCTCG	GGCCAGAAGG	GCGGTACCG	AGGAGCTGCC	GGATTGTTTG	60
------------	-----------	------------	-----------	------------	------------	----

GCAACGGGCGG GGCCTGGNGGT GCTGGGCGGCT CCAACCAAGC CGCTAACGGC GGNCGCGGCG 120
GAAACGGTGG TGCCCGCTGG CTGATCTG 149

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGCACGAGA TCACACCTAC CGAGTGAATG AGATCGTGG GACCTCGCCC GACGGTGTGG 60
ACGCGGNAAT CCAGGGCGGT CTGGCTUGAG CTGCGGAGAC CATCGGCGCG CTGGACTGGT 120
TCGAATACA CTCAATTGGA GGCCACCTGG TCGACGGAGC GGTGGGGCAC TTCCAGGTGA 180
CTATGAAAT CGGCTTCGGC CTGGAGGATT CCTGAACCTT CAAGCGCGGC CATAACTGA 240
GGTGATCAT TAAGCGACTT TTCCAGAACA TCCTGACGGC CTCGAAAGCC GGTTCAGCCG 300
ACGGTGGCTC CGCCGAGGCG CTGCTCCAA AATCCGTGG ACAATTGCTC GGCGG 355

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCAC ATCAACATCA CATGCATCAG GTGGACDCCA ACTTGACAGG TCCCAAGGGA 60
CGATTGGCGG CACTGGGTAT CGCGGCGATG GCDAGCCCA GCTGGGTGAC GGTTCGGGTS 120
CCCGGACCG CCACGGCGGA TCCGAGCCA GCGCCCCCGG TACCCACAAC GGGCGGCTCG 180
CGCCGCTCGA CGGCTGCAGC GCAACCGCA CCGGCGACAC CTGTTGGCCC CCAACACCG 240
GGCGCGCCA ACACGCGAA TCGCCAGCG GCGATCCCA ACGCAGCACC TCGCGGGCC 300
GACCCGACG CACCGCGCC ACCTGTCAAT GCGCCAAAG CACCCGACC TGTCCGATC 360
GACACCGCG TTGGAGGATT CAGCTTGGCG CTGCTGCTG GCTGGGTGCA CTCTGACGG 420
GCGCACTTCG ACTACGGTC AGCACTCTC AGCAAAACA CCGGGGACCC GCGATTTCG 480
GGACAGCGC CGCGGTGGC CATGACACC CGTATCGTG TCGCCCGCT AGACCAAAG 540


```

CTTTACGCCA GCGCCCAAGC CACCGACTCC AAGGCCCGCG CCCGCTTGGC CTCGGACATG      600
GGTGAGTTCT ATATGCCCTA CCGGGGCACC CGGATCAACC AGGAAGCCTT CTCGCTCGAC      660
GCCAACGGGG TGTCTGGAAG CGCGTCGTAT TACGAAGTCA AGTTCAGCGA TCCGASTAAG      720
CCGAACGGGC AGATCTGGAC GGGCGTATC GGCTCSCCCG CCGCGAAGCG ACCCGACGCG      780
GGCCCCCTTC AGCGCTGGTT TGTGGTATGG CTCGGGACCG CCAACAACCC GGTGGACAAG      840
GGCGCGGGCA AGCGCTGGC CGAATCGATC CCGCCTTTGG TCGCCCGCGC GCUGGCGCGC      900
GCACCGGCTC CTCGAGAGCC CGCTCCGGCG CCGCGCGCGG CTCGGGAGT CGCTCTAC      960
CCGACGACAC CGACACCGCA GCGGACCTTA CCGGCTGA      999

```

(2) INFORMATION FOR SEQ ID NO:53:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(a) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Met His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1           5           10           15

Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20           25           30

Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35           40           45

Gln Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50           55           60

Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65           70           75           80

Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85           90           95

Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
100          105          110

Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
115          120          125

Phe Ala Leu Pro Ala Gly Trp Val Gln Ser Asp Ala Ala His Phe Asp
130          135          140

Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
145          150          155          160

Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
165          170          175

```

```

Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
    180                                185                                190
Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
    195                                200                                205
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
    210                                215                                220
Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
    225                                230                                235                                240
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
    245                                250                                255
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
    260                                265                                270
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Gln
    275                                280                                285
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
    290                                295                                300
Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Gln Val Ala Pro Thr
    305                                310                                315                                320
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
    325                                330

```

(2) INFORMATION FOR SEQ ID NO:54:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(21) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Xaa Asn Tyr Gly Gln Val
1           5           10           15
Val Ala Ala Leu
    20

```

(2) INFORMATION FOR SEQ ID NO:55:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Val	Gln	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:56:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1			5						10						15

Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:57:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr	Tyr	Trp	Cys	Pro	Gly	Glu	Pro	Phe	Asp	Pro	Ala	Trp	Gly	Pro
1			5						10					15

(2) INFORMATION FOR SEQ ID NO:58:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp	Ile	Gly	Ser	Glu	Ser	Thr	Glu	Asp	Gln	Gln	Asa	Ala	Val
1			5						10				

(2) INFORMATION FOR SEQ ID NO:59:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala	Glu	Glu	Ser	Ile	Ser	Thr	Xaa	Glu	Xaa	Ile	Val	Pro
1				5							10	

(2) INFORMATION FOR SEQ ID NO:60:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp	Pro	Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Ala	Ala	Ala	Ala	Pro	Pro
1				5					10					15	

Ala

(2) INFORMATION FOR SEQ ID NO:61:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala	Pro	Lys	Thr	Tyr	Xaa	Glu	Glu	Leu	Lys	Gly	Thr	Asp	Thr	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:62:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln	Gln	Thr	Ser
1			5						10					15	
Leu	Leu	Asn	Asn	Leu	Ala	Asp	Pro	Asp	Val	Ser	Phe	Ala	Asp		
		20					25						30		

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Thr	Gly	Ser	Leu	Asn	Gln	Thr	His	Asn	Arg	Arg	Ala	Asn	Glu	Arg	Lys
1			5						10					15	
Asn	Thr	Thr	Met	Lys	Met	Val	Lys	Ser	Ile	Ala	Ala	Gly	Leu	Thr	Ala
			20				25						30		
Ala	Ala	Ala	Ile	Gly	Ala	Ala	Ala	Ala	Gly	Val	Thr	Ser	Ile	Met	Ala
		35				40						45			
Gly	Gly	Pro	Val	Val	Tyr	Gln	Met	Gln	Pro	Val	Val	Phe	Gly	Ala	Pro
	50				55						60				
Leu	Pro	Leu	Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln
65					70				75						80
Leu	Thr	Ser	Leu	Leu	Asn	Ser	Leu	Ala	Asp	Pro	Asn	Val	Ser	Phe	Ala
			85						90					95	
Asn	Lys	Gly	Ser	Leu	Val	Glu	Gly	Gly	Ile	Gly	Gly	Thr	Glu	Ala	Arg
			100				105						110		
Ile	Ala	Asp	His	Lys	Leu	Lys	Lys	Ala	Ala	Glu	His	Gly	Asp	Leu	Pro
		115				120						125			
Leu	Ser	Phe	Ser	Val	Thr	Asn	Ile	Gln	Pro	Ala	Ala	Ala	Gly	Ser	Ala
		130				135					140				
Thr	Ala	Asp	Val	Ser	Val	Ser	Gly	Pro	Lys	Leu	Ser	Ser	Pro	Val	Thr
145					150					155					160
Gln	Asn	Val	Thr	Phe	Val	Asn	Gln	Gly	Gly	Trp	Met	Leu	Ser	Arg	Ala
			165					170						175	
Ser	Ala	Met	Glu	Leu	Leu	Gln	Ala	Ala	Gly	Asa					
		180						185							

(2) INFORMATION FOR SEQ ID NO:64:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
1           5           10           15
Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser
20           25           30
Gly Val Gln Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
35           40           45
Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser
50           55           60
Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val
65           70           75           80
Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val
85           90           95
Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val
100          105          110
Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu
115          120          125
Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser
130          135          140
Thr Gly Gly Pro
145

```

(2) INFORMATION FOR SEQ ID NO:65:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr
1           5           10           15
Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln
20           25           30

```

```

Gln Arg Asp Ala Leu Cys Leu Ser Ser Thr Gln Ile Ser Arg Gln Ser
  35                               40                               45

Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn
  50                               55                               60

Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu
  65                               70                               75                               80

Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Gln
  85                               90                               95

Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser
 100                               105                               110

Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp
 115                               120                               125

Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu
 130                               135                               140

Ser Ala Ala Thr Ser Ser Thr Pro Arg Glu Ala Pro Tyr Glu Leu Asn
 145                               150                               155                               160

Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln
 165                               170                               175

Ala Val Val Leu Xaa Val Tyr His Asn Ala Gly Gly Thr His Pro Thr
 180                               185                               190

Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile
 195                               200                               205

Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val
 210                               215                               220

Phe Pro Ile Val Ala Arg
 225                               230

```

(2) INFORMATION FOR SEQ ID NO:66:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1           5           10           15

Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20           25           30

Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35           40           45

```

98

```

Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50                      55                      60

Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65                      70                      75                      80

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85                      90                      95

Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100                      105                      110

Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Gln
115                      120                      125

Gly Pro Pro Ala
130

```

(2) INFORMATION FOR SEQ ID NO:67:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
 1                      5                      10                      15

Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Arg Leu Ser Asn Pro Pro
20                      25                      30

Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
35                      40                      45

Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
50                      55                      60

Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
65                      70                      75                      80

Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
85                      90                      95

Ser Gln Arg Lys
100

```

(2) INFORMATION FOR SEQ ID NO:68:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
1      5      10      15
Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
20     25     30
Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
35     40     45
Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
50     55     60
Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
65     70     75     80
Thr Ala Val Gly Gly His Asp Glu Ala Gly Asp Arg Arg Asp Gln Arg
85     90     95
Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
100    105    110
Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
115    120    125
Ala Ala Ala His Leu Gly Thr Glu Cys Val Leu Ala Ala Lys Gly Arg
130    135    140
His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg
145    150    155    160
Asp Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
1      5      10      15
Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
20     25     30
Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
35     40     45

```

100

Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Gln Val Pro
 50 55 60
 Arg Gly Arg Lys Gln Ala Val Ala Ala Val Ala Ala Ser Leu Arg
 65 70 75 80
 Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly
 85 90 95
 Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Gly Thr Ala Pro Ala Ala
 100 105 110
 Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr
 115 120 125
 Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Gln Tyr
 130 135 140
 Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val
 145 150 155 160
 Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu
 165 170 175
 Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Gln
 180 185 190
 His Arg Pro Gly Arg Ser Thr Arg Arg Leu Gln Pro Arg Thr Leu Pro
 195 200 205
 Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe
 210 215 220
 Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro
 225 230 235 240
 Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Gln Pro
 245 250 255
 Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Gln Leu Pro
 260 265 270
 Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala
 275 280 285
 Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu
 290 295 300
 Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr
 305 310 315 320
 Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Gln Gly Gln
 325 330 335
 Val Ser Arg Gln Asn Pro Thr Gly
 340

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 amino acids

(B) TYPE: amino acid

101

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp	Asp	Pro	Asp	Met	Pro	Gly	Thr	Val	Ala	Lys	Ala	Val	Ala	Asp	Ala	1	5	10	15
Leu	Gly	Arg	Gly	Ile	Ala	Pro	Val	Glu	Asp	Ile	Gln	Asp	Cys	Val	Glu	20	25	30	
Ala	Arg	Leu	Gly	Glu	Ala	Gly	Leu	Asp	Asp	Val	Ala	Arg	Val	Tyr	Ile	35	40	45	
Ile	Tyr	Arg	Gln	Arg	Arg	Ala	Glu	Leu	Arg	Thr	Ala	Lys	Ala	Leu	Leu	50	55	60	
Gly	Val	Arg	Asp	Glu	Leu	Lys	Leu	Ser	Leu	Ala	Ala	Val	Thr	Val	Leu	65	70	75	80
Arg	Glu	Arg	Tyr	Leu	Leu	His	Asp	Glu	Gln	Gly	Arg	Pro	Ala	Glu	Ser	85	90	95	
Thr	Gly	Gln	Leu	Met	Asp	Arg	Ser	Ala	Arg	Cys	Val	Ala	Ala	Ala	Glu	100	105	110	
Asp	Gln	Tyr	Glu	Pro	Gly	Ser	Ser	Arg	Arg	Trp	Ala	Gln	Arg	Phe	Ala	115	120	125	
Thr	Leu	Leu	Arg	Asn	Leu	Glu	Phe	Leu	Pro	Asn	Ser	Pro	Thr	Leu	Met	130	135	140	
Asn	Ser	Gly	Thr	Asp	Leu	Gly	Leu	Leu	Ala	Gly	Cys	Phe	Val	Leu	Pro	145	150	155	160
Ile	Gln	Asp	Ser	Leu	Gln	Ser	Ile	Phe	Ala	Thr	Leu	Gly	Gln	Ala	Ala	165	170	175	
Glu	Leu	Gln	Arg	Ala	Gly	Gly	Gly	Thr	Gly	Tyr	Ala	Phe	Ser	His	Leu	180	185	190	
Arg	Pro	Ala	Gly	Asp	Arg	Val	Ala	Ser	Thr	Gly	Gly	Thr	Ala	Ser	Gly	195	200	205	
Pro	Val	Ser	Phe	Leu	Arg	Leu	Tyr	Asp	Ser	Ala	Ala	Gly	Val	Val	Ser	210	215	220	
Met	Gly	Gly	Arg	Arg	Arg	Gly	Ala	Cys	Met	Ala	Val	Leu	Asp	Val	Ser	225	230	235	240
His	Pro	Asp	Ile	Cys	Asp	Phe	Val	Thr	Ala	Lys	Ala	Glu	Ser	Pro	Ser	245	250	255	
Glu	Leu	Pro	His	Phe	Asn	Leu	Ser	Val	Gly	Val	Thr	Asp	Ala	Phe	Leu	260	265	270	
Arg	Ala	Val	Glu	Arg	Asn	Gly	Leu	His	Arg	Leu	Val	Asn	Pro	Arg	Thr	275	280	285	

Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile
 290 295 300
 Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp
 305 310 315 320
 Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala
 325 330 335
 Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn
 340 345 350
 Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp
 355 360 365
 Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp
 370 375 380
 Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala
 385 390 395 400
 Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu
 405 410 415
 Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg
 420 425 430
 Leu Ala Thr Arg Leu Met Arg Arg Ile Glu Glu Ala Ala His Thr Ala
 435 440 445
 Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp
 450 455 460
 Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Glu Val Thr Ser
 465 470 475 480
 Val Ala Pro Thr Gly
 485

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu
 1 5 10 15
 Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val
 20 25 30
 Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala
 35 40 45

```

Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His
 55          55          60
Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu
 65          70          75          80
Gly Asn Ala Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Glu Thr Pro
      85          90          95
Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Glu Gly Asp
      100          105          110
Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
      115          120          125
Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn
      130          135          140
Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
      145          150          155          160
Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp
      165          170          175
Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu
      180          185          190
Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg
      195          200          205
Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val
      210          215          220
Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn
      225          230          235          240
Gln Pro Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln
      245          250          255
Ala Pro Pro Pro Glu Ser Pro Ala Gln Gly Gly
      260          265

```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
1           5           10           15
Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala
      20           25           30

```

104

Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr
 35 40 45
 Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
 50 55 60
 Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp
 65 70 75 80
 Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu
 85 90 95
 Gln

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 364 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala
 1 5 10 15
 Cys Gly Gly Gly Thr Asn Ser Ser Ser Ser Gly Ala Gly Gly Thr Ser
 20 25 30
 Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser
 35 40 45
 Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
 50 55 60
 Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
 65 70 75 80
 Gly Val Thr Glu Phe Leu Asn Asn Gln Thr Asp Phe Ala Gly Ser Asp
 85 90 95
 Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg
 100 105 110
 Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala
 115 120 125
 Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro
 130 135 140
 Thr Thr Ala Lys Ile Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro
 145 150 155 160
 Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile
 165 170 175

105

Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln
 180 185 190
 Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser
 195 200 205
 Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly
 210 215 220
 Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Gln
 225 230 235 240
 Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr
 245 250 255
 Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
 260 265 270
 Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu
 275 280 285
 Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile
 290 295 300
 Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr
 305 310 315 320
 Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly
 325 330 335
 Gln Gln Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe
 340 345 350
 Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser
 355 360

(2) INFORMATION FOR SEQ ID NO:74:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp
 1 5 10 15
 Gln Thr His Gln Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val
 20 25 30
 Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro
 35 40 45
 Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser
 50 55 60

106

Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg
 65 70 75 80
 Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro
 85 90 95
 Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg
 100 105 110
 Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp
 115 120 125
 Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val
 130 135 140
 Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg
 145 150 155 160
 Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly
 165 170 175
 Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala
 180 185 190
 Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val
 195 200 205
 Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg
 210 215 220
 Ala Gly Pro Gln Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro
 225 230 235 240
 Leu Pro Ala Arg Ala Gly Gln Gln Gln Pro Ser Ser Ala Gly Gly Arg
 245 250 255
 Arg Ala Gly Gly Ala Glu Arg Ala Asp Pro Gly Gln Arg Gly Arg His
 260 265 270
 His Gln Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr
 275 280 285
 Ala Gly Val Ala His Ala Ala Ala Gly Pro Arg Arg Ala Ala Val Arg
 290 295 300
 Asn Arg Pro Arg Arg
 305

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 580 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

107

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly
 1 5 10 15
 Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys
 20 25 30
 Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala
 35 40 45
 Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys
 50 55 60
 Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr
 65 70 75 80
 Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser
 85 90 95
 Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His
 100 105 110
 Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Gln
 115 120 125
 Glu Glu Gln Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro
 130 135 140
 Pro Gln Gln Pro Gly Thr Pro Gly Tyr Ala Gln Gly Gln Gln Gln Thr
 145 150 155 160
 Tyr Ser Gln Gln Phe Asp Trp Arg Tyr Pro Pro Ser Pro Pro Pro Gln
 165 170 175
 Pro Thr Gln Tyr Arg Gln Pro Tyr Glu Ala Leu Gly Gly Thr Arg Pro
 180 185 190
 Gly Leu Ile Pro Gly Val Ile Pro Thr Met Thr Pro Pro Pro Gly Met
 195 200 205
 Val Arg Gln Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr
 210 215 220
 Ile Ala Val Val Ser Ala Gly Ile Gly Gly Ala Ala Ala Ser Leu Val
 225 230 235 240
 Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala
 245 250 255
 Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val
 260 265 270
 Glu Gln Val Ala Ala Lys Val Val Pro Ser Val Val Met Leu Glu Thr
 275 280 285
 Asp Leu Gly Arg Gln Ser Glu Glu Gly Ser Gly Ile Ile Leu Ser Ala
 290 295 300
 Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Ala Lys
 305 310 315 320
 Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp

	325		330		335
Gly Arg Thr Ala	Pro Phe Thr Val	Val Gly Ala Asp	Pro Thr Ser Asp		
	340	345	350		
Ile Ala Val Val	Arg Val Gln Gly	Val Ser Gly Leu	Thr Pro Ile Ser		
	355	360	365		
Leu Gly Ser Ser	Ser Asp Leu Arg	Val Gly Gln	Pro Val Leu Ala Ile		
	370	375	380		
Gly Ser Pro Leu	Gly Leu Gln Gly	Thr Val Thr Thr	Gly Ile Val Ser		
	385	390	395	400	
Ala Leu Asn Arg	Pro Val Ser Thr	Thr Gly Gln Ala	Gly Asn Gln Asn		
	405	410	415		
Thr Val Leu Asp	Ala Ile Gln Thr	Asp Ala Ala Ile	Asn Pro Gly Asn		
	420	425	430		
Ser Gly Gly Ala	Leu Val Asn Met	Asn Ala Gln Leu	Val Gly Val Asn		
	435	440	445		
Ser Ala Ile Ala	Thr Leu Gly Ala	Asp Ser Ala Asp	Ala Gln Ser Gly		
	450	455	460		
Ser Ile Gly Leu	Gly Phe Ala Ile	Pro Val Asp	Gln Ala Lys Arg Ile		
	465	470	475	480	
Ala Asp Gln Leu	Ile Ser Thr Gly	Lys Ala Ser	Hie Ala Ser Leu Gly		
	485	490	495		
Val Gln Val Thr	Asn Asp Lys Asp	Thr Pro Gly	Ala Lys Ile Val Gln		
	500	505	510		
Val Val Ala Gly	Gly Ala Ala Ala	Asn Ala Gly	Val Pro Lys Gly Val		
	515	520	525		
Val Val Thr Lys	Val Asp Asp Arg	Pro Ile Asn	Ser Ala Asp Ala Leu		
	530	535	540		
Val Ala Ala Val	Arg Ser Lys Ala	Pro Gly Ala	Thr Val Ala Leu Thr		
	545	550	555	560	
Phe Gln Asp	Pro Ser Gly Gly	Ser Arg Thr	Val Gln Val Thr	Leu Gly	
	565	570	575		
Lys Ala Gln Gln					
	580				

(2) INFORMATION FOR SEQ ID NO:76:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 233 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu
1      5      10
Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro
20     25     30
Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro
35     40     45
Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu
50     55     60
Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu
65     70     75     80
Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Leu Ala
85     90     95
Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly Val Pro Phe Arg
100    105    110
Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn
115    120    125
Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala
130    135    140
Ala Gly Val Thr Glu Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln
145    150    155    160
Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr
165    170    175
Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala
180    185    190
Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val
195    200    205
Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Glu Leu Thr Gln Ser
210    215    220
Lys Trp Asn Glu Pro Val Asn Val Asp
225    230

```

(2) INFORMATION FOR SEQ ID NO:77:

```

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala

```

110

```

1           5           10           15
Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
20           25           30
Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
35           40           45
Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
50           55           60
Pro Arg
65

```

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser
1           5           10           15
Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
20           25           30
Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro
35           40           45
Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
50           55           60
Ser Pro Pro Leu Pro
65

```

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
1           5           10           15
Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
20           25           30

```

III

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Gln Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Gln Gln Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Gln Gly
 340 345 350
 Pro Pro Ala

355

(2) INFORMATION FOR SEQ ID NO:80:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Ser Pro Lys Pro Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr
1           5           10           15
Ala Ser Asp Pro Ala Leu Leu Ala Gln Ile Arg Gln Ser Leu Asp Ala
20           25           30
Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys
35           40           45
Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala
50           55           60
Asp Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly
65           70           75           80
Val Pro Phe Arg Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp
85           90           95
Asp Trp Ser Asn Leu Gly Ser Ile Ser Gln Leu Ser Thr Thr Arg Val
100          105          110
Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn
115          120          125
Leu Gln Ala Gln Gly Thr Gln Val Ile Asp Gly Ile Ser Thr Thr Lys
130          135          140
Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly
145          150          155          160
Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser
165          170          175
His His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln
180          185          190
Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp
195          200          205

```

(2) INFORMATION FOR SEQ ID NO:81:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly	Asp	Ser	Phe	Trp	Ala	Ala	Ala	Asp	Gln	Met	Ala	Arg	Gly	Phe	Val	1	5	10	15
Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu	Thr	Gly	Glu	Gly	Leu	Gln	20	25	30	
His	Ala	Asp	Gly	His	Ser	Leu	Leu	Leu	Asp	Ala	Thr	Asn	Pro	Ala	Val	35	40	45	
Val	Ala	Tyr	Asp	Pro	Ala	Phe	Ala	Tyr	Glu	Ile	Gly	Tyr	Ile	Xaa	Glu	50	55	60	
Ser	Gly	Leu	Ala	Arg	Met	Cys	Gly	Glu	Asn	Pro	Glu	Asn	Ile	Phe	Phe	65	70	75	80
Tyr	Ile	Thr	Val	Tyr	Asn	Glu	Pro	Tyr	Val	Gln	Pro	Pro	Glu	Pro	Glu	85	90	95	
Asn	Phe	Asp	Pro	Glu	Gly	Val	Leu	Gly	Gly	Ile	Tyr	Arg	Tyr	His	Ala	100	105	110	
Ala	Thr	Glu	Gln	Arg	Thr	Asn	Lys	Xaa	Gln	Ile	Leu	Ala	Ser	Gly	Val	115	120	125	
Ala	Met	Pro	Ala	Ala	Leu	Arg	Ala	Ala	Gln	Met	Leu	Ala	Ala	Glu	Trp	130	135	140	
Asp	Val	Ala	Ala	Asp	Val	Trp	Ser	Val	Thr	Ser	Trp	Gly	Glu	Leu	Asn	145	150	155	160
Arg	Asp	Gly	Val	Val	Ile	Glu	Thr	Glu	Lys	Leu	Arg	His	Pro	Asp	Arg	165	170	175	
Pro	Ala	Gly	Val	Pro	Tyr	Val	Thr	Arg	Ala	Leu	Gln	Asn	Ala	Arg	Gly	180	185	190	
Pro	Val	Ile	Ala	Val	Ser	Asp	Trp	Met	Arg	Ala	Val	Pro	Glu	Gln	Ile	195	200	205	
Arg	Pro	Trp	Val	Pro	Gly	Thr	Tyr	Leu	Thr	Leu	Gly	Thr	Asp	Gly	Phe	210	215	220	
Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Gly	Arg	Arg	Tyr	Phe	Asn	Thr	Asp	225	230	235	240
Ala	Glu	Ser	Gln	Val	Gly	Arg	Gly	Phe	Gly	Arg	Gly	Trp	Pro	Gly	Arg	245	250	255	
Arg	Val	Asn	Ile	Asp	Pro	Phe	Gly	Ala	Gly	Arg	Gly	Pro	Pro	Ala	Gln	260	265	270	
Leu	Pro	Gly	Phe	Asp	Glu	Gly	Gly	Gly	Leu	Arg	Pro	Xaa	Lys	275	280	285			

(2) INFORMATION FOR SEQ ID NO:82:

114

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr
1      5      10      15
Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp
20      25      30
Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg
35      40      45
Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg
50      55      60
Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro
65      70      75      80
Arg Glu Ala Leu Ala Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp
85      90      95
Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Gln Gly Asp Phe Leu
100     105     110
Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Gln Gln Ile Glu Glu Val
115     120     125
Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn
130     135     140
Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro
145     150     155     160
Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu
165     170

```

(2) INFORMATION FOR SEQ ID NO:83:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile
1      5      10      15

```


115

```

Ala Ala Gly Leu Thr Ala Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly
  20                      25                      30
Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro
  35                      40                      45
Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa
  50                      55                      60
Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp
  65                      70                      75                      80
Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Glu Gly Gly Ile
  85                      90                      95
Gly Gly Xaa Glu Gly Xaa Xaa Arg Arg Xaa Gln
 100                      105

```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn
 1      5      10      15
Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr
 20      25      30
Arg Arg Ala Leu Glu Leu Gln Ala Pro Ser Val Val Xaa Arg Gln Gly
 35      40      45
Val Lys Glu Pro Leu Xaa Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
 50      55      60
Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
 65      70      75      80
Gly Lys Asn Arg Arg Leu Cys Arg Thr Pro Ser Ser Asn Gln Arg Gln
 85      90      95
Gln Leu Gly Val Arg Trp Ile Pro Arg Ser Arg Cys Ala Cys Val Tyr
100      105      110
Val Gly His Arg Ala Arg Arg Gly Thr Tyr His Arg Arg
115      120      125

```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

116

(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

Cys Asp Ala Val Met Gly Phe Leu Gly Gly Ala Gly Pro Leu Ala Val
 1           5           10           15
Val Asp Gln Gln Leu Val Thr Arg Val Pro Gln Gly Trp Ser Phe Ala
 20           25           30
Gln Ala Ala Ala Val Pro Val Val Phe Leu Thr Ala Trp Tyr Gly Leu
 35           40           45
Ala Asp Leu Ala Gln Ile Lys Ala Gly Glu Ser Val Leu Ile His Ala
 50           55           60
Gly Thr Gly Gly Val Gly Met Ala Ala Val Gln Leu Ala Arg Gln Trp
 65           70           75           80
Gly Val Gln Val Phe Val Thr Ala Ser Arg Gly Lys Trp Asp Thr Leu
 85           90           95
Arg Ala Xaa Xaa Phe Asp Asp Xaa Pro Tyr Arg Xaa Phe Pro His Xaa
100           105           110
Arg Ser Ser Xaa Gly
115

```

(2) INFORMATION FOR SEQ ID NO:86:

```

(1) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 103 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

```

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu
 1           5           10           15
Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln
 20           25           30
Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Glu Pro Phe Asp
 35           40           45
Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
 50           55           60
His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
 65           70           75           80
Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro

```

117

85

90

95

Pro Ala Ala Gly Gly Gly Ala
100

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Val Gln Cys Arg Val Trp Leu Glu Ile Gln Trp Arg Gly Met Leu Gly
1 5 10 15
Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His
20 25 30
Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala
35 40 45
Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly
50 55 60
Gly Arg Leu Val Val Glu Leu Thr Pro Asp Glu Ala Ala Ala Leu Gly
65 70 75 80
Asp Glu Leu Lys Gly Val Thr Ser
85

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
1 5 10 15
Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
20 25 30
Ser Leu Glu Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
35 40 45
Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
50 55 60

118

```

Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
65              70              75              80

Ala Asp Glu Gln Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
85              90              95

```

(2) INFORMATION FOR SEQ ID NO:89:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Gln Ile Leu Asn
1              5              10              15

Arg Ala Asn Glu Val Gln Ala Pro Met Ala Asp Pro Pro Thr Asp Val
20              25              30

Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln
35              40              45

Xaa Val Leu Ser Ala Asp Asn Met Arg Gln Tyr Leu Ala Ala Gly Ala
50              55              60

Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
65              70              75              80

Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
85              90              95

Gln Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100             105             110

Ser Ala Gln Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
115             120             125

Asp Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
130             135             140

Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr
145             150             155             160

Leu Thr Leu Gln Gly Asp
165

```

(2) INFORMATION FOR SEQ ID NO:90:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

[xi] SEQUENCE DESCRIPTION: SEQ ID NO:90:

Arg Ala Glu Arg Met
1 5

(2) INFORMATION FOR SEQ ID NO: 51:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

{21} SEQUENCE DESCRIPTION: SEQ ID NO:91:

Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	Ala	1
5									10						15	
Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	Thr	20
25													30			
Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	Leu	35
40							40					45				
Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	Asn	50
55						55					60					
Gln	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	Phe	65
70					70					75					80	
Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro	Phe	85
90					85				90					95		
Gln	Gln	Ala	Pro	Gln	Met	Thr	Ser	Ala	Gly	Gly	Leu	Leu	Glu	Gln	Ala	100
105			100					105					110			
Ala	Ala	Val	Gln	Glu	Ala	Ser	Asp	Thr	Ala	Ala	Ala	Asn	Gln	Leu	Met	115
120							120					125				
Asn	Asn	Val	Pro	Gln	Ala	Leu	Lys	Gln	Leu	Ala	Gln	Pro	Thr	Gln	Gly	130
135						135					140					
Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	Leu	Trp	Lys	Thr	Val	Ser	Pro	145
150					150					155					160	
His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	Ser	Met	Ala	Asn	Asn	His	Met	165
170				165					170					175		
Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	Thr	Asn	Thr	Leu	Ser	Ser	Met	180
185			180					185					190			
Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	Ala	Gln	Ala	Val	Gln	Thr	Ala	195
200						200						205				

120

Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
 210 215 220

Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
 225 230 235 240

Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Asn Ser Gly
 245 250 255

Arg Arg Asn Gly Gly Pro Ala
 260

(2) INFORMATION FOR SEQ ID NO:92:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(a1) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala
 1 5 10 15

Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Gln Gly
 20 25 30

Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly
 35 40 45

Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr
 50 55 60

Gln Leu Gly Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro
 65 70 75 80

Val Gly Val Ala Leu Leu Ala Ala Leu Leu Ala Gly Val Val Leu Val
 85 90 95

Pro Lys Ala Lys Ser His Val Thr Val Val Ala Val Leu Gly Val Leu
 100 105 110

Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr
 115 120 125

Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln
 130 135 140

Ala Val Ala Ala Val Leu Ala Leu Leu Val Gln Thr Gly Ala Ile Thr
 145 150 155 160

Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg
 165 170 175

Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr Tyr Gly
 180 185 190

121

```

Gln Gln Gly Ala Gln Gln Ala Ala Gly Leu Gln Ser Pro Gly Pro Gln
 195                      200                      205
Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Gly Tyr Ser
 210                      215                      220
Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Pro Ala
 225                      230                      235                      240
Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser
 245                      250                      255
Thr Pro Pro Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Pro Val Ser
 260                      265                      270
Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn
 275                      280                      285
Pro Ser Gly Gly Gln Gln Ser Ser Ser Pro Gly Gly Ala Pro Val
 290                      295                      300

```

(2) INFORMATION FOR SEQ ID NO:93:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```

Gly Cys Gly Gln Thr Asp Ala Ala Thr Leu Ala Gln Gln Ala Gly Asn
 1           5           10           15
Phe Gln Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile
 20           25

```

(2) INFORMATION FOR SEQ ID NO:94:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```

Asp Gln Val Gln Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly
 1           5           10           15

```

(2) INFORMATION FOR SEQ ID NO:95:

- (1) SEQUENCE CHARACTERISTICS:

122

(A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

Gly Cys Gly Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala
1           5           10           15
Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
20           25

```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

Gly Cys Gly Gly Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu
1           5           10           15
Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu
20           25

```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```

Gly Cys Gly Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr
1           5           10           15
Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
20           25

```

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly	Cys	Gly	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser	Arg	Ala	Asp	Gln
1				5				10						15	
Glu	Gln	Gln	Gln	Ala	Leu	Ser	Ser	Gln	Met	Gly	Phe				
			20					25							

(2) INFORMATION FOR SEQ ID NO:99:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 507 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAAGATGG	TGAAATCGAT	CGCCCGCAGGT	CTGACCCGCG	CGGCTGCAAT	CGGCGCCGCT	60
CGGCGCCGCTG	TGACTTCGAT	CATGGCTGGC	GGCCCGGTGG	TATACCAGAT	GCAGCCGCTC	120
GTCTTCGGGG	CGGCACTGCC	GTGGGACCGC	GCATCCGGCC	CTGACGTTCC	GACCGCGGCC	180
CAGTTGACCA	GGCTGCTCAA	CAGGCTCGCC	GATCCCAAGG	TGTCGTTTGC	GAACAGGGGC	240
AGTCTGGTCC	AGGGCGGCAT	CGGGGGCACC	GAGGCGCGCA	TCCCGSACCA	CAAGCTGAAG	300
AAGGCCGCGC	AGCAGGGGGA	TCTGCCGCTG	TGGTTCAGCG	TGACGACAT	CCAGCCGGCG	360
GCAGCCGGTT	CGGCGACCGC	CGAGTTTTCG	GTCTCGGGTC	CGAAGCTCTC	GTGCGCGGTC	420
ACGCAAGAAC	TACGTTCTGT	GAATCAAGGC	GGCTGGATGC	TGTCACGGCG	ATCGGCGATC	480
GAGTTGCTGC	AGGCGCGCAG	GAACTGA				507

(2) INFORMATION FOR SEQ ID NO:100:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

124

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala
 1 5 10 15
 Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro
 20 25 30
 Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu
 35 40 45
 Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
 50 55 60
 Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly
 65 70 75 80
 Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg Ile Ala Asp
 85 90 95
 His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe
 100 105 110
 Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp
 115 120 125
 Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Glu Asn Val
 130 135 140
 Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met
 145 150 155 160
 Glu Leu Leu Gln Ala Ala Gly Asn
 165

(2) INFORMATION FOR SEQ ID NO:101:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CGTGGCAATG TCGTTGACCG TCGGGGCCCCG GGTGGGCTCC GCAGATCCCG TGGACGCGGT 60
 CATTAAACACC ACCTGCAATT ACGGGCAGGT AGTAGCTGCG CTCACGCGCA CGGATCCGGG 120
 GGCTGCCGCA CAGTTCACCG CCTCACCGTT GCGGCAGTCC TATTTGCCCA ATTCTCTGCG 180
 CCGACCGGCA CCTCAGGCGG CTGCCATGGC CCGGCAATTG CAAGCTGTGC CCGGGGCGCGC 240
 ACAGTACATC GGCCTGTCTG AGTGGTTTC CCGCTCTCTC AACCACTATT AAGCCCCATGC 300
 GGGCCCATC CCGCGACCGG GCATCTGTGC CCGGGCTAGG CCAGATTGCC CCGCTCTCA 360
 ACGGGCGGCA TCCCGCGACC CGGCATCTTC GCGGGGGCTA GCGCAGATTG CCGGCTCTCT 420
 CACCGGGGCG CATCTCTCTC CGAATTCTG CAGCCCCGGG GATCCACTAG TTCTAGAGCG 480

GDCGCCACCG CGGTGGAGCT

500

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Val	Ala	Met	Ser	Leu	Thr	Val	Gly	Ala	Gly	Val	Ala	Ser	Ala	Asp	Pro
1				5					10					15	
Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Val	Ala
			20					25					30		
Ala	Leu	Asn	Ala	Thr	Asp	Pro	Gly	Ala	Ala	Ala	Gln	Phe	Asn	Ala	Ser
			35				40					45			
Pro	Val	Ala	Gln	Ser	Tyr	Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro
			50			55				60					
Gln	Arg	Ala	Ala	Met	Ala	Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala
65				70					75					80	
Gln	Tyr	Ile	Gly	Leu	Val	Glu	Ser	Val	Ala	Gly	Ser	Cys	Asn	Asn	Tyr
			85					90					95		

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGACAGAGC	AGCAGTGGAA	TTTCGCGGCT	ATCGAGGCCG	CGGCAAGCC	AATCCAGGGA	60
AATGTCACGT	CCATTCATTC	CCTCCTTGAC	GAGGGGAAGC	AGTCCCTGAC	CAAGCTGCCA	120
GCCTGCTGGG	GCGGTAGCGG	TTGGAAGCG	TACC			154

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
 1           5           10           15

Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
 20           25           30

Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
 35           40           45

Glu Ala Tyr
 50

```

(2) INFORMATION FOR SEQ ID NO:195:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

CGGTCCGGCA CTTCACGTC ACTATGAAAC TCGGCTTCCG NOTGCAGGAT TCTGAACTT      60
TCAGGCGCGG CGATAACTG AGGTGCATCA TTAGCCGACT TTTCCAGAAC ATCCTGACGC      120
GCTCGAAAGC CGGCACAGCC GACGGTGGCT CGGCGGAGGC GCTGCTCCCA AAATCCCTGA      180
GACAAATTCG CCGGGGCGGC TACAAGGAAG TCGGTGCTGA ATTCCGCGCG TATCTGGTGG      240
ACCTGTGTGG TCTGNAGCCG GACGAGCGCG TCGTCGACGT CG                        282

```

(2) INFORMATION FOR SEQ ID NO:196:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3058 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

GATCGTACCC GTGGAGTGC TCGGGCGGTT TCAGGATGGA GTGCACGTGT CTTTCGTGAT      60
GGCATACCCA GAGATGTTGG CCGCGGCGGC TGACACCTTG CAGAGCATCG GTGCTACAC      120
TGTGGCTAGC AATGCCGCTG CCGCGGCCCC GACGACTGGG GTGTTGCCCC CCGCTGCCCA      180

```

TCAGGTGTCC	GCCTGACTG	CGCCGCACTT	CGCCGACAT	CCGCGCATGT	ATCAATCCGT	240
GAGCGTCCG	GCTGCTGCA	TTCATGACCA	GTTCGTGGCC	ACCTTTGCCA	GCACGCCAG	300
CTCGTATGCG	GCCACTGAAG	TCCCAATGC	GGCGCGGCC	AGCTAAGCCA	GGAACAGTCC	360
GCACGAGAAA	CCACGAGAAA	TAGGGACACG	TAATGCTGGA	TTTCGGGGCG	TTACACCCCG	420
AGATCAACTC	CGCGAGGATG	TACGCCGGCC	CGGTTCCGG	CTCGCTGGTG	GCCGCGGCTC	480
AGATGTGGGA	CAGCGTGGCG	AGTACCTGT	TTTCGGGCCG	GTGGGCTTTT	CAGTCGGTGG	540
TCCTGGGTCT	GACGTTGGGG	TGGTGATAG	GTTCGTGGCG	GGGTCTCATG	GTGGCGGCGG	600
CTTCGCCGTA	TGTGGCTGG	ATGAGCTCA	CCGCGGGCA	GGCGAGCTG	ACCGCGGCC	660
AGGTCCGGGT	TGCTGCGGCG	GCTACGAGA	CGGCTATGG	GCTGACGGTG	CCCCCGCCGG	720
TGATCGCCGA	GAACCTGCT	GAACTGATGA	TTCTGATAGC	GACCAACCTC	TTGGGGCAAA	780
ACACCCCGGC	GATCGCGGTC	AACGAGGCCG	ATACCGCGA	GATGTGGGCC	CAAGACGCCG	840
CCGCGATGTT	TGGCTACGCC	GCGCGACCG	CGACGGCGAC	GGGAGGTTG	CTCCCTTCG	900
AGGAGGCGCC	GGAGTGAAC	AGCGCGGGTG	GGCTCTCGA	GCAGGCGGCC	GCGGTCGAGG	960
AGGCTCCGA	CACCGCGCG	GCGAACCACT	TGATGAACAA	TGTGCCCCAG	GCGCTGCAAC	1020
AGCTGGCCCA	GCCGACGGAG	GGCACCAAGC	CTTCTTCCAA	GCTGGTGGC	CTGTGGAAGA	1080
CGGTCTCGCC	GCATCGGTGG	CCGATCGCA	ACATGGTCTC	GATGSCCAAC	AACCACATGT	1140
CGATGACCAA	CTCGGTGTG	TGGATGACCA	ACACCTTGAG	CTCGATGTTG	AAAGGCTTTG	1200
CTCGGCGCG	GGCGCGCGG	GCGGTGCAAA	CGCGGCGCA	AAACGGGGTC	CGGCGCATGA	1260
GCTCGCTGGG	CAGCTGGCTG	GTTCTTCCG	GTCTGGGCGG	TGGGTGGCC	GCCAACTTGG	1320
GTGGGCGCG	CTCGGTGGGT	TGTTTGTGG	TGCGCGAGGC	CTGGCGCGCG	GCCAACGAGG	1380
CAGTCACCCC	GGCGGCGCG	GCGCTGCGGC	TGACCAAGCTT	GACCAAGCGC	GCGGAAAGAG	1440
GGCGCGGGCA	GATGCTGGGC	GGGCTGCCGG	TGGGCGAGAT	GGGCGCCAGG	GCGGTGGTG	1500
GGCTCAGTGG	TGTGCTGGGT	GTTCGCGGCG	GACCTATGTT	GATGCGCGAT	TCTCGGCGCG	1560
CCGCTAGGA	GAGGGGGCGC	AGACTGTGCT	TATTTGACCA	GTGATCGCGG	GTCTCGGTGT	1620
TTCCGCGGCC	GGCTATGACA	ACAGTCAATG	TGATGACAA	GTTACAGGTA	TTAGGTCCAG	1680
GTTCAACAAG	GAGACAGGCA	ACATGCGCTC	ACUTTTTATG	ACGATTCGGC	ACGCGATGCG	1740
GGACATGGCG	GCCCGTTTTG	AGGTGCACGC	CCAGACGGTG	GAGGACGAGG	CTCGCGGGAT	1800
GTGGGCGTCC	GCGCAAAACA	TTTCGGGTGC	GGGCTGGAGT	GGCATGGCGG	AGGCGACCTC	1860
GCTAGACACC	ATGGGCCAGA	TGAATCAGGC	GTTTCGCAAC	ATGCTGAACA	TGCTGCACCG	1920
GGTGGGTGAC	GGGCTGGTTC	GCGACGCCAA	CABCTACGAG	CAGCGAGAGC	AGGCTTCCCA	1980
GCAGATCCTC	AGCACTAAC	GTGAGCGGCT	GCAGCACAAZ	ACTTTTACAA	GCGAGGAGAA	2040

```

ACAGSTTCCA TGACCATCAA CTATCAATTC GGGGATSTCG ACGCTCACGG CGCCATGATC 2100
CGCCCTCAGG CCGGCTTCTT GGAGGCCCGAG CATTAGGCCA TCATTCTGTA TGTCTTGACU 2160
GGGAGTGAAT TTTGGGGCGG CCGCCGTTTG GCGGCTGCGC AGGGGTTTAT TACCCAGTTG 2220
GGCCCTAATC TCCAGGTGAT CTACGAGCAG GCCAACGCCC ACGGGCAGAA GGTGCAGGCT 2280
GGCGGCAACA ACATGGCCCA AACCGACAGC GCGCTCGGCT CCAGCTGGGC CTGACACCCAG 2340
GCCAAGGCCA GGGACGTGGT GTACGAGTGA AATTCTCTGC GTGATCCTTC GGTTCGCACT 2400
CTAAGTGGTC AGTGGTGGG TGTGGTGGT TTGCTGCTTG GCGGTTCTT CHTGCTGGT 2460
CAGTCTCTCT CCGGCTCGGG TGAGGACCTC GAGGCCGAGG TAGCGCCGTC CTTCGATCCA 2520
TTCTCTCTCT TGTTCGGGCA GGACGGCTTC GAGGAGGCGG ATGATCGAGG CGCGGTCGGG 2580
GAAGATGCCC ACACGCTGGG TTGGGGGTTC TACTCTCGG TTGAGGGCTT CCTGGGGGTT 2640
GTTGGACCAG ATTTGGCCGC ACATCTGCTT GGGGAGGCGC GTGAACGCCA GCAGGTCGGT 2700
CGGGGGGGTG TCGAGGTGCT CCGCCACCGC GGGGAGTTTG TCGGTCAGAG CGTCGAGTAC 2760
CCGATCATAT TGGGCAACAA CTGATTCGGC GTGGGGCTTG TCGTAGATGG AGTCCAGCAG 2820
GGTGGCCACC CACGGCCAGG AGGGCTTCGG GGTGGCTGCC ATCAGATTGG CTGGGTAGTG 2880
GTTTCTGCAG CGCTGCCAGG CGCTGCGGG CAGGTTGGCG CCGATCGCGG CCACCAGGCC 2940
GGCGTGGCGG TCGCTGGTGA CCAGCGCGAC CCGGACAGG CCGCGGCGA CCAGGTCGCG 3000
GAAGAACGCC AGCCAGCGGG CCGGCTCTC GCGGAGGCTG ACCTGATGCG CCAGGATC 3058

```

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asp Ser Ala Arg Met
1           5           10           15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
20           25           30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
35           40           45
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
50           55           60
Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr

```

129

65		70		75		80
Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala	85		90		95	
Ala Tyr Gln Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala	100		105		110	
Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly	115		120		125	
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met	130		135		140	
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala	145		150		155	160
Thr Ala Thr Ala Thr Leu Leu Pro Phe Gln Glu Ala Pro Gln Met Thr	165		170		175	
Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser	180		185		190	
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu	195		200		205	
Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu	210		215		220	
Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn	225		230		235	240
Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val	245		250		255	
Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala	260		265		270	
Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala	275		280		285	
Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly	290		295		300	
Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val	305		310		315	320
Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg	325		330		335	
Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly	340		345		350	
Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly	355		360		365	
Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met	370		375		380	
Pro His Ser Pro Ala Ala Gly	385		390			

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1725 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

GACCTCAGCA CCCGCCGTGC AGGCTGGAG CTTGGTCGGT TTTGATCTGC GGTCAAGGTG      60
ACGTCCCTCG GCGTGTCCGC GGGTGGATG CAGACTCGAT GCGCTCTTT AGTGCAACTA      120
ATTTCCTTGA AGTGCCTCG AGGTATAGGA CTTCAAGATT GGTAAATGTA GCGTTCACCC      180
CGTCTTGGGG TCGATTTCGC CGGACCAGTC GTACCAACG CTTGGCCTGC GCGCCAGGCG      240
GGGATCAGA TCGCTTGAAT ACCAATCAAT CTGAGCTCC CCGCCCGATG CTCGGGCTAA      300
ATGAGGAGGA GCAGCGCTGT CTTTCACTGC GCAACGGGAG ATGTTGGCG GCGCGGCTGG      360
CGAAGTTGCT TCCCTGGGGG CAACGCTGAA GGCTAGCAAT GCGGCGCAG CCGTGGCGAC      420
GACTGGGGTG GTGCCCCCGG CTGCGACGA GGTGTGGCTG CTGCTTGGCA CACAATTCCG      480
TACGCATGCG GCGAGGTATC AGACGGCCAG CGCAAGCCC GCGGTGATCC ATGAGCAATT      540
TGTGACCACG CTGGCCACCA GGGTAGTTC ATATCGGGAC ACCGAGGCCG CCAACGCTGT      600
GGTCACCGGC TAGCTGACCT GACGCTATTC CAGCGGAAGG ATTATCGAAG TGGTGGATTG      660
CGGGGCGTTA CCACCGGAGA TCAACTCCGC GAGGATGTAC GCGGCCCCGG GTTCGGCTTC      720
GCTGCTGGCC GCGGCAAGA TGTGGGACAG CGTGGCGAGT GACCTGTTTT CCGCCGCGTC      780
GGCGTTTCAG TCGTGGTCT GGGTCTGAC GGTGGGCTCG TGGATAGCTT CGTCGGCGGG      840
TCTGATGGCG GCGGCGGCTT CGCGTATGT GCGTGGATG AGCGTCACCG CCGGGCAGGC      900
CCAGCTGACC GCGGCGCAG TCCGGGTTGC TCGGGGGGCC TACGAGACAG CGTATAGGCT      960
GAGGTTGCCC CCGCGGGTGA TCGCGAGAA CGTACCGAA CTGATGACGC TGACCGCGAC      1020
CAACCTCTTG GGGCAAAACA CGCGGCGAT CGAGGCCAAT CAGGCGCAT ACAGCCAGAT      1080
GTGGGGGCAA GACGCGGAGC CGATGTATGG CTACGCGCC ACGGCGGGA CCGCGACCGA      1140
GGGTTGCTG CCGTTCGAGG ACGGCGCACT GATCAGCAAC CCGGCGGGG TCCTTGASCA      1200
GGCGTTCGCG GTCGAGGAGG CCATCGACAC CCGCGCGGG AACCAATTGA TGAACAATGT      1260
GCGGCAAGCG CTGCAACAGC TGGGCGAGC AGCGAGGCG GTGTTACCTT CTTCGAAGCT      1320
GGGTGGGCTG TGGAGGCGCG TCTCGCGCA TCTGTGCGG CTCAGCAACG TCACTTCGAT      1380
AGCCAACAAC CACATGTGGA TGATGGGCAC GGTGTGTGCG ATGACCAACA CCTTGCCTC      1440

```



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GATGTTGAAG GGCTTAGCTC CGGCGGCGGC TCAGGCGCTG GAACCCGCGG CCGAAAACGG 1500
GGTCTGGGCG ATGAGCTGCC TGGGCAGCCA GTTGGGTTCC TCGCTGGGTT CTTCGGGTCT 1560
GGGCGCTGGG GTGGCCGCCA ACTTGGGTCC GCGCGCCTCC GTGGGTTGTT TGTGGGTGCC 1620
GCCAGCATGG GCGCGGCCCA ACCAGCGCGT CACCCCGGCG GCGCGGCGCG TCCCGCTGAC 1680
CAGCCTGACC AGCGCGGCGC AAACCGCCCG CGGACACATC CTGGG 1725

```

(2) INFORMATION FOR SEQ ID NO:169:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```

Val Val Asp Phe Gly Ala Leu Pro Pro Gln Ile Asn Ser Ala Arg Met
1      5      10      15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
20     25     30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
35     40     45
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
50     55     60
Leu Met Ala Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65     70     75     80
Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
85     90     95
Ala Tyr Gln Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala
100    105    110
Gln Asn Arg Thr Gln Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly
115    120    125
Gln Asn Thr Pro Ala Ile Gln Ala Asn Gln Ala Ala Tyr Ser Gln Met
130    135    140
Trp Gly Gln Asp Ala Gln Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala
145    150    155    160
Thr Ala Thr Gln Ala Leu Leu Pro Phe Gln Asp Ala Pro Leu Ile Thr
165    170    175
Asn Pro Gly Gly Leu Leu Gln Gln Ala Val Ala Val Gln Gln Ala Ile
180    185    190
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
195    200    205

```

Gln Gln Leu Ala Gln Pro Ala Gln Gly Val Val Pro Ser Ser Lys Leu
 210 215 220

Gly Gly Leu Trp Thr Ala Val Ser Pro His Leu Ser Pro Leu Ser Asn
 225 230 235 240

Val Ser Ser Ile Ala Asn Asn His Met Ser Met Met Gly Thr Gly Val
 245 250 255

Ser Met Thr Asn Thr Leu His Ser Met Leu Lys Gly Leu Ala Pro Ala
 260 265 270

Ala Ala Gln Ala Val Glu Thr Ala Ala Glu Asn Gly Val Trp Ala Met
 275 280 285

Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu
 290 295 300

Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser
 305 310 315 320

Leu Ser Val Pro Pro Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro
 325 330 335

Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr
 340 345 350

Ala Pro Gly His Met Leu Gly
 355

(2) INFORMATION FOR SEQ ID NO:110:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(*1) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AGTTCAGTCG AGRATGATAC TGACGGGCTG TATCCACGAT GGCTGAGACA ACCGAACCAC 60

CGTCGGACGC GGGACATCG CAAGCCGACG CGATGGCTT GGGGCGCGAA GCGAAGCCG 120

CGAAGCCGA AGCGTGCGC GCGCGGCGC GGGCCCTGC CCGTGGCGC CGGTGAGGC 180

GTGAGGCGCT GCGATGCGC CCGCGGAGG ACGAGACGT CCGGAGGAT ATGCAGACTG 240

GGAGAGCGCC GAAGACTATG ACGACTATGA CGACTATGAG GCGGAGAGC AGGAGCGCG 300

ACGGTCGGCA TCCTGGCGAC GCGGTTGCG CGTGGGTTA CCGAGACTGT CCACGATTGC 360

CATGCGCGCG CGAGTGGTCA TCATCTGCGG CTTCAACGGG CTCAGCGGAT ACATTGTGTG 420

GCAACACCAT GAGGCTACCG AACGTCAGCA GCGGCGCGG GCGTTGCGG CCGGAGCCGA 480

CCAGGTGTC ATCAACATGA CCTCGCTGGA CTTCAACAAG GCCAAGAGG ACCTCGCGCG 540

TGTGATCGAC	AGCTCCACCG	GCGAATTCAG	GGATGACTTC	CAGCAGCCGG	CAGCCGATTT	600
CACCAAGGTT	GTCCGACAGT	CCAAAGTGGT	CACCGAGGCG	ACGGTGAACG	CGACAGCCGT	660
CGAATCCATG	AACGAGCAAT	CCGCCGTGGT	GCTCGTGGCG	GCGACTTCAC	GGGTACCCAA	720
TTCCGCTGGG	GCGAAGAGCG	AACCACGTGC	GTGGCGGGCTC	AAAGTGACCG	TGACCGAAGA	780
GGGGGGACAG	TACAAGATGT	CGAAAGTTGA	GTTGGTACCG	TGACCGATGA	CGTACCGGAC	840
GTCAPCAECG	AAACCACTGA	CGCCACCGAA	GTCGCTGAGA	TGGACTCAGC	CGCAGGCCAA	900
GCGGGTGATT	CGGCCACCGA	GGCATTTGAC	ACCGACTCTG	CAACGGAATC	TACCGCGGAG	960
AAGGGTCAGC	GGCACCGTGA	CCTGTGCGGA	ATGCAGGTTA	CCTTGAACC	CGTTCCGGTG	1020
ATTCTCTATC	TGCTCATGTT	GATCTCTGGG	GGGCGGACCG	GATGGCTATA	CCTTGAGCAA	1080
TACGACCCGA	TCAGCAGACG	GACTCGGGCG	CGGCGCGTGC	TGCGGTGCGC	GCGGCGTCTG	1140
ACGGGACAAAT	CGCGCTGTTG	TGTATTCAAC	CGACACGTGC	ACCAAGACTT	CCCTACCCGC	1200
AGGTGCGAAC	TGCGCGCGGA	TTTCTGTGCC	TATACGACCA	GTTCAAGCAG	CAGATCGTGG	1260
CTCGGCGCGC	CAACAGAGAG	TCACTGAAAA	CCACCGCCAA	GGTGGTGCGC	GCGGCGGTGT	1320
CGGAGCTACA	TCCGGATTGG	GCCTGCTTC	TGGTTTTTGT	CGACCAAGGC	ACTACCAGTA	1380
AGGACAGCCC	CAATCCGTGG	ATGGGCGCCA	GCAGCGTGAAT	GGTGACCTTA	GCCAAGGTGG	1440
ACGGCAATG	GCTGATCACC	AAGTTCACCC	CGGTTTAGGT	TGCGGTAGGC	GGTCCGCCAG	1500
TCTGACGGGG	GCSCGGGTGG	CTGCTCGTGC	GAGTACCCGG	CGTTTCTCCG	GACAATCAGC	1560
GCCCGACCTC	AAACAGATCT	CGGCCGCTGT	CTAATCGGCG	CGGTTATTTA	AGATTAGTTG	1620
CCACTGTATT	TACCTGATGT	TCAGATTGTT	CAGCTGGATT	TAGCTTCGCG	GCGGGGCGGC	1680
TGGTGCACTT	TGCATCTGGG	GTTGTGACTA	CITGAGAGAA	TTTGAACCTGT	TGCGACGTTT	1740
GTTTGTCTGT	CATCATGGGT	GCTAGTTATG	GCCGAGCGGA	AGGATTATCG	AAGTGGTGA	1800
CTTGGGGGCG	TTACCAACCG	AGATCAACTC	CGCGAGGATG	TACGCGGGCG	CGGTTTCCGC	1860
CTCGCTGGTG	GCCGCCCGGA	AGATGTGGGA	CAGGCTGGCG	AGTGACCTGT	TTTCCGGCGC	1920
GTGCGCGTTT	CAGTGGGTGG	TCTGGGCTCT	GACGAGCGGA	TGTTGGATAG	GTTGCTCGGC	1980
GGTCTGATG	GTGGCGGCGG	CTTCCCGGTA	TGTGGCGTGG	ATGAGCGTCA	CCCGGGGGCA	2040
GGCGGAGCTG	ACCGCGGGCG	AGGTCCGGGT	TGCTGCGGCG	GCCTACGAGA	CGGCGTATGG	2100
GCTGACGGTG	CCCCCGCCCG	TGATCGCCGA	GAACCGTGCT	GAACTGATGA	TTCTGATAGC	2160
GACCAACCTC	TTGGGGCAAA	ACACCCCGGC	GATCGCGGTC	AACGAGGCGG	AATACGGGGA	2220
GATGTGGGCG	CAAGACGCGG	CCGCGATGTT	TGGTACCGCG	GCCACGGGCG	CGACGGCGAC	2280
CGAGCGGTTG	CTGCGGTTGG	AGGACGCCCC	ACTGATCACC	AACCCCGGCG	GGCTCCTTGA	2340
GCAGGCGGTC	GCGGTGGAGG	AGGCCATCGA	CACGCGCGCG	GCGAACCACT	TGATGAACAA	2400

134

```

TGTGCCCCAA GCGCTGCAAC AACTGGCCCA GCCCACGAAA AGCATCTGGC CTTTCGACCA 2460
ACTGAGTGAA CTCTGGAAAG CCACTCTGCC GCATCTGTTC CCGCTCAGCA ACATCGTGTG 2520
GATGCTCAAC AACCACGTGT CGATGACCAA CTCGGGTGTG TCGATGSCCA GCACCTTGCA 2580
CTCAATGTTG AAGGGCTTTG CTCGGGCGGC GGCCTCAGGC GTGGAAACCG CGGCCGAAA 2640
CGGGGTCCAG CGCATGAGCT CGCTGGGCAG CCAGCTGGGT TCGTGGCTGG GTTCTTCGGG 2700
TCTGGGCGCT GGGGTGGCCG CCAACTTGGG TCGGGCGGCC TCGGTGSGTT CGTTGTGGT 2760
GCCGACGGCC TGGGCGGGGG CCAACCAGGC GGTGACGCGG GCGGCGCGGG CGCTGCGGCT 2820
GACGAGCTTG ACCAGCGCCG CCCAAACCGC CCGCGGACAC ATGCTGGGCG GGTACCGCT 2880
GGGGCAACTG ACCAATAGCG GCGGCGGGTT CGGCGGGGTT AGCAATGGT TCGGATGCC 2940
GCCGCGGGCG TACGTATGC CCGTGTGCC CCGCGCGGGG TAACGCGGAT CCGCACGCAA 3000
TGGGGGCCCT CTATGCGGCG AGCGATC 3027

```

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1           5           10           15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
20           25           30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
35           40           45
Val Val Trp Gly Leu Thr Thr Gly Ser Trp Ile Gly Ser Ser Ala Gly
50           55           60
Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65           70           75           80
Ala Gly Glu Ala Glu Leu Thr Ala Ala Glu Val Arg Val Ala Ala Ala
85           90           95
Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
100          105          110
Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
115          120          125
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met

```

135

130	135	140
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Thr Ala Ala 145 150 155 160		
Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr 165 170 175		
Asn Pro Gly Gly Leu Leu Gln Gln Ala Val Ala Val Glu Glu Ala Ile 180 185 190		
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu 195 200 205		
Gln Gln Leu Ala Gln Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu 210 215 220		
Ser Glu Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn 225 230 235 240		
Ile Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val 245 250 255		
Ser Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala 260 265 270		
Ala Ala Gln Ala Val Glu Thr Ala Ala Gln Asn Gly Val Gln Ala Met 275 280 285		
Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu 290 295 300		
Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser 305 310 315 320		
Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro 325 330 335		
Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr 340 345 350		
Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn 355 360 365		
Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro 370 375 380		
Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly 385 390 395		

(2) INFORMATION FOR SEQ ID NO:112:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1616 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(1) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATCGGAGGG AGTGATCACC ATGCTGTGGC AGGCAATGCC ACCGGAGTAA ATACCGCACC	60
GCTGATGGGC GCGCGGGGTC CGGCTCCAAT GCTTCGGGCG SCCGCGGGAT GGCAGACGCT	120
TTGCGCGGCT CTGGACGCTC AGGCGGTGCA GTTGACCGCG CCGCTGAACCT CTCTGGGAGA	180
AGCCTGGACT GGAGGTGGCA GCGACAAGGC GCTTCGGGCT GCAACGCCGA TGCTGGTCTG	240
GCTACAAACC GCTCAACAC AGGCCAAGAC CCGTGGGATG CAGGCGACCG CGCAAGCGGC	300
GGCATAACCC CAGGCGATCG CCACGACGCG GTGCGTGGCG GAGATCGCGG CCAACACAT	360
CACCCAGGGC GTCCCTACGG CCACCAACTT CTTGCGTATC AACACGATCC CGATCGGCTT	420
GACCGAGATG GATTATTTCA TCGGTATGTC GAACGAGGCA GCGCTGGCAA TGGAGGTCTA	480
CCAGGCGCGG ACCCGGGTTA ACACGCTTTT CGAGAAGCTC GAGCGGATGG CTTGATCTCT	540
TGATCCCGGC GCGAGCCAGA GCACGACGAA CCGATCTTC GGAATGCCCT CCGCTGGCAG	600
CTCAACACCG GTTGGCCACT TGGCGCGGCG GGTACCCAG ACCCTCGGCG AACTGGGTGA	660
GATGAGCGGC CCGATGCAGC AGCTGACCCA GCGGCTGCGG CAGGTGACGT GGTGTTTCAG	720
CCAGGTGGGC GGCACCGGCG GCGGCAACCC AGCGGACGAG GAAGCCGCGC AGATGGGCTT	780
GCTCGGCACC AGTCCGCTGT CGAACCTATC GCTGGCTGGT GGATCAGGCC CCAGCGCGGG	840
CGCGGGGCTG CTGCGCGCGG AGTCCCTACC TGGCGCAGGT GGGTGGTTGA CCGGACGCGC	900
GCTGATGTCT CAGCTGATCG AAAAGCCGGT TCGCCCTCTG GTGATGCCGG CCGCTGCTGC	960
CGGATCGTCC GCGACGGGTG GCGCCGCTCC GGTGGGTGCG GGAGCGATGG GCCAGGGTGC	1020
GCAATCCGCG GGTCCACCA GCGCGGTCTT GGTGCGGCGG GCACCGCTCG CGCAGGAGCG	1080
TGAAGAGAC GACGAGGACG ACTGGGACGA AGAGGACGAC TGGTGAGCTC CCGTAATGAC	1140
AACAGACTTC CCGGCCACCC GGGCGGGAG ACTTCCCAAC ATTTTGGCGA GGAAGGTAAA	1200
GAGAGAAAGT ACTCCAGCAT GGCAGAGATG AAGACGATG CCGCTACCTT CCGCGAGGAG	1260
GCAGGTAATT TCGAGCGGAT CTCGCGCGAC CTGAAAACCC AGATCGACCA GGTGGAGTCC	1320
ACGGCAGGTT CGTTGCAGGG CCAGTGGCGC GCGCGGCGCG GGACGGCGCG CCAGGCCGCG	1380
GTGTTGGCTT TCCAGAGAGC AGCCAATAAG CAGAAGCAGG AACTCGACGA GATCTCGACG	1440
AATATTCGTC AGGCCGGGCT CCAATACTCG AGGGCGGAGG AGGAGCAGCA GCAGGCGCTG	1500
TCCTCGCAAB TGGGCTTCTG ACCCGCTAAT ACGAAAAGAA ACGGAGCAAA AACATGACAG	1560
AGCAGCACTG GAATTTGCGG GGTATCGAGG CCGCGGCAAG CCGAATCCAG GCAAAAT	1616

(2) INFORMATION FOR SEQ ID NO:113:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```

CTACTGGATG GGACCATGGC CATTTCCTGC AGTCTCACTG CTTCTCTGTG TGACATTTTC      60
GCACGCGCGG GGAACGAAAG CACTGGGGTC GAASRACGGC TCGGCTGCCA TATCGTCCGG      120
AGCTTCCATA CTTTCGTCCG GCCGGAAGAG CTTCTCTGAG TCGGCGGCCA TGACAACCTC      180
TCAGAGTGCG CTCAAACGTA TAAACACGAG AAGGCTCGAG ACCGACGCAA GGTCGAACTC      240
GCCCGATCCC GTGTTTCGGT ATTCTACGGC AACTCGGCGT TCGGCTATGC GAACATCCCA      300
GTACAGTTCG CTTGGGTCCA AGCCATTGCC TGACCGGCTT CGCTGATCGT CCGCGCCAGG      360
TTCTGCAGCG CGTTCCTCAG CTCGGTAGCC GTGGCGTCCC ATTTTTCCTG GACACCCCTG      420
TACGCTTCGG AA                                     432

```

(2) INFORMATION FOR SEQ ID NO:114:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```

Met Leu Trp His Ala Met Pro Pro Gln Xaa Asn Thr Ala Arg Leu Met
1           5           10           15
Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Ala Gly Trp Gln
20           25           30
Thr Leu Ser Ala Ala Leu Asp Ala Gln Ala Val Glu Leu Thr Ala Arg
35           40           45
Leu Asn Ser Leu Gly Glu Ala Trp Thr Gly Gly Gly Ser Asp Lys Ala
50           55           60
Leu Ala Ala Ala Thr Pro Met Val Val Trp Leu Gln Thr Ala Ser Thr
65           70           75           80
Gln Ala Lys Thr Arg Ala Met Gln Ala Thr Ala Gln Ala Ala Ala Tyr
85           90           95
Thr Gln Ala Met Ala Thr Thr Pro Ser Leu Pro Glu Ile Ala Ala Asn
100          105          110
His Ile Thr Gln Ala Val Leu Thr Ala Thr Asn Phe Phe Gly Ile Asn
115          120          125

```

138

```

Thr Ile Pro Ile Ala Leu Thr Glu Met Asp Tyr Phe Ile Arg Met Trp
130                      135                      140

Asn Gln Ala Ala Leu Ala Met Glu Val Tyr Gln Ala Gln Thr Ala Val
145                      150                      155                      160

Asn Thr Leu Phe Glu Lys Leu Glu Pro Met Ala Ser Ile Leu Asp Pro
165                      170                      175

Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro
180                      185                      190

Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr
195                      200                      205

Leu Gly Gln Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln
210                      215                      220

Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly
225                      230                      235                      240

Gly Gly Asn Pro Ala Asp Glu Glu Ala Ala Gln Met Gly Leu Leu Gly
245                      250                      255

Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Gly Ser Gly Pro Ser
260                      265                      270

Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly
275                      280                      285

Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val
290                      295                      300

Ala Pro Ser Val Met Pro Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly
305                      310                      315                      320

Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser
325                      330                      335

Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln
340                      345                      350

Glu Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp
355                      360                      365

```

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
1           5           10           15

```


139

```

Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
      20                      25                      30
Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
      35                      40                      45
Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
      50                      55                      60
Gln Lys Gln Glu Leu Asp Gln Ile Ser Thr Asn Ile Arg Gln Ala Gly
      65                      70                      75                      80
Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser
      85                      90                      95
Gln Met Gly Phe
      100

```

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```

GATCTCCGGC GACCTGAAA CCCAGATCGA CCAGGTGGAG TCGACGGCAG GTTCGTTCGA      60
GGGCCAGTGG CGGGGCGCGG CCGGACGGC CCCCCAGGCC GCGGTGGTGC GCTTCCAAGA      120
AGCAGCCCAT AACCAAGAGC AGGAATCTGA CGAGATCTCG ACCAATATTC CTCAGGCCGG      180
CCTCCAATAC TCGAGGGCCG ACCAGGAGCA GCAGCAGGCG CTGTCTCTCG AAATGGGCTT      240
CTGACCGGCT AATACGAAA GAAACGGAGC AAAAACATGA CAGAGCAGCA GTGGAATTTT      300
GCGGCTATCG AGGCCGCGC AACGCCAATC CAGGAAATG TCAGTCCAT TCATTCCCTC      360
CTTGACGAGG GGAAGCAGTC CCTGACCAAG CTCGCA                                396

```

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```

Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala

```

140

1	5	10	15
Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln	20	25	30
Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu	35	40	45
Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser	50	55	60
Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe	65	70	75
			80

(2) INFORMATION FOR SEQ ID NO:118:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(*1) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```

GTGGATCCCG ATCCGCTGTT TCGCTATTCT ACACGAACCTC GGCCTTCCCC TATGCGAACA      60
TCCAGTGCAC GTTGCCCTTCG CTCGAAGCCA TTGCCTGACG GGTTCGCTG ATCGTCCGCG      120
CCAGGTTCTG CAGCGCGTTG TTCAGCTCGG TAGCCGTGGC GTCCCATTTT TCCTGACAC      180
CCTGCTACSC CTCGGAACCG CTACGCGCCC AGGCCGCTGC GAGCTTGGTC AGGGAAGTCT      240
TCCCTTCGTC AAGGAGGAAA TGAATGGAGC TGACATTTCC CTGGATTGCG CTTGCGCGCG      300
CCTCGATAAC CCGGAATTC CACTGCTGCT CTGTCAATGT TTGCTCCGT TTCTTTTCGT      360
ATTAGCGGCT CAGAAGCCCA TTTCGCA

```

(2) INFORMATION FOR SEQ ID NO:119:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(*1) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```

CGGCACGAGG ATCTCGGTTG GCGCAACGCG GCTGCGGAGG GCTCCCTTCC GCGGCGGAGC      60
TGCGCGCCCG ATGCTTCTTC TGCCCGCAGC CGCCTCTGCA TCGATGGACC AGTTGCTACC      120
TTCCCGACST TTCGTTGGGT GTCTGTGCGA TACGCGTGAC CCGGCGCGCG ACCTCGGAG      180

```

TGTTGGGGGG CAGCCCGGGT CGGTGGTTCC GCGGGGGGAG CAGACGGTCT GGACGGAACG 240
 GCGGGGGGTT CCGCGATTGG CATCTTTGCC CA 272

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val
 1 5 10 15
 Val Ala Ala Leu
 20

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala Val Gln Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys
 1 5 10 15
 Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	She	Asp	Pro	Ala	Trp	Gly	Pro
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp	Ile	Gly	Ser	Glu	Ser	Thr	Glu	Asp	Glu	Gln	Xaa	Ala	Val
1				5					10				

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Ala	Glu	Glu	Ser	Ile	Ser	Thr	Xaa	Glu	Xaa	Ile	Val	Pro
1				5					10			

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro
1          5          10          15
Ser

```

(2) INFORMATION FOR SEQ ID NO:127:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
1          5          10          15

```

(2) INFORMATION FOR SEQ ID NO:128:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Glu Leu Thr Ser
1          5          10          15

Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn
          20          25          30

```

(2) INFORMATION FOR SEQ ID NO:129:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```

Asp Pro Pro Asp Pro His Gln Xaa Asp Met Thr Lys Gly Tyr Tyr Pro
1          5          10          15

```